

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: August 14, 2006, 21:51:58 ; Search time 49 Seconds
(without alignments)
239.369 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711
Sequence: 1 MCGQDRHMRRLDIDVDQ.....LLQRMHQLSRTGSEDS 134.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /EMC_Celerra_SIDS3/prodata/2/1aa/5 COMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/1aa/6 COMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/1aa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/8 COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/1aa/9 COMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/1aa/10 COMB.pep.*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	99.3	162	2	US-09-522-217-2 Sequence 2, Appl.
2	706	99.3	162	2	US-09-923-246-2 Sequence 2, Appl.
3	706	99.3	162	2	US-10-295-723-2 Sequence 2, Appl.
4	706	99.3	162	2	US-08-825-561A-10 Sequence 10, Appl.
5	706	99.3	162	2	US-10-282-622-2 Sequence 2, Appl.
6	706	99.3	174	2	US-09-949-016-10307 Sequence 10307, A
7	695	97.7	519	2	US-09-522-217-85 Sequence 85, Appl.
8	695	97.7	519	2	US-09-923-246-85 Sequence 85, Appl.
9	695	97.7	519	2	US-10-295-723-85 Sequence 85, Appl.
10	694	97.6	162	2	US-10-282-622-6 Sequence 6, Appl.
11	621	87.3	147	2	US-10-282-622-4 Sequence 4, Appl.
12	404	56.8	146	2	US-09-522-217-56 Sequence 56, Appl.
13	404	56.8	146	2	US-09-923-246-56 Sequence 56, Appl.
14	404	56.8	146	2	US-10-295-723-56 Sequence 56, Appl.
15	404	56.8	146	2	US-08-825-561A-47 Sequence 47, Appl.
16	394	55.4	510	2	US-09-522-217-89 Sequence 89, Appl.
17	394	55.4	510	2	US-09-923-246-89 Sequence 89, Appl.
18	394	55.4	510	2	US-10-295-723-89 Sequence 89, Appl.
19	212	29.8	40	2	US-09-522-217-72 Sequence 72, Appl.
20	212	29.8	40	2	US-09-923-246-72 Sequence 72, Appl.
21	212	29.8	40	2	US-10-295-723-72 Sequence 72, Appl.
22	176	24.8	32	2	US-08-522-217-73 Sequence 73, Appl.
23	176	24.8	32	2	US-09-923-246-73 Sequence 73, Appl.
24	176	24.8	32	2	US-10-295-723-73 Sequence 73, Appl.
25	99.5	14.0	114	1	US-08-031-399-6 Sequence 6, Appl.
26	99.5	14.0	114	1	US-08-031-399-12 Sequence 12, Appl.

27	99.5	14.0	114	1	US-08-393-305-3 Sequence 3, Appl.
28	99.5	14.0	114	1	US-08-726-817-3 Sequence 3, Appl.
29	99.5	14.0	114	1	US-08-504-042-6 Sequence 6, Appl.
30	99.5	14.0	114	1	US-08-504-042-12 Sequence 12, Appl.
31	99.5	14.0	114	1	US-08-725-969-3 Sequence 3, Appl.
32	99.5	14.0	114	1	US-08-794-524-3 Sequence 3, Appl.
33	99.5	14.0	114	2	US-09-189-193-3 Sequence 3, Appl.
34	99.5	14.0	114	2	US-09-462-941-40 Sequence 20, Appl.
35	99.5	14.0	114	5	PCT-US94-03793-6 Sequence 6, Appl.
36	99.5	14.0	114	5	PCT-US94-03793-12 Sequence 12, Appl.
37	99.5	14.0	162	1	US-08-031-399-5 Sequence 5, Appl.
38	99.5	14.0	162	1	US-08-393-305-2 Sequence 2, Appl.
39	99.5	14.0	162	1	US-08-535-733-2 Sequence 2, Appl.
40	99.5	14.0	162	1	US-08-726-817-2 Sequence 2, Appl.
41	99.5	14.0	162	1	US-08-504-042-5 Sequence 5, Appl.
42	99.5	14.0	162	1	US-08-725-969-2 Sequence 2, Appl.
43	99.5	14.0	162	1	US-08-794-524-2 Sequence 2, Appl.
44	99.5	14.0	162	1	US-08-842-947-6 Sequence 6, Appl.
45	99.5	14.0	162	2	US-09-189-193-2 Sequence 2, Appl.

ALIGNMENTS

RESULT 1
US-09-522-217-2
Sequence 2, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Preenell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Groes, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Tracey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT FILING DATE: 2000-03-09
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-2

Query Match 99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	CGQDRHMRRLDIDVDQKRYNDLVPRFLPPEVETNCESASCPKAKLKANT	61
DB	30	CGQDRHMRRLDIDVDQKRYNDLVPRFLPPEVETNCESASCPKAKLKANT	89
QY	62	GNRRITIVSIKKLKRKPSTNAGROKRLTCCSCSYKKPKFLERFKSLIQMII	121
DB	90	GNRRITIVSIKKLKRKPSTNAGROKRLTCCSCSYKKPKFLERFKSLIQMII	149
QY	122	QHSRTGSEDS 134	
DB	150	QHSRTGSEDS 162	

THIS PAGE LEFT BLANK

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:51:58 ; Search time 49 Seconds

(without alignments)
239.369 Million cell updates/sec

Title: US-10-735-149-28

Sequence: 1 MGGDRHMRQLDIDVQ.....LQGMHQLSSRTGSEDS 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	99.3	162	2	US-09-522-217-2 Sequence 2, Appli
2	706	99.3	162	2	US-09-923-246-2 Sequence 2, Appli
3	706	99.3	162	2	US-10-295-723-2 Sequence 2, Appli
4	706	99.3	162	2	US-09-825-561A-10 Sequence 10, Appli
5	706	99.3	162	2	US-10-282-622-2 Sequence 2, Appli
6	706	99.3	174	2	US-09-949-016-10307 Sequence 10307, A
7	695	97.7	519	2	US-09-522-217-85 Sequence 85, Appli
8	695	97.7	519	2	US-09-923-246-85 Sequence 85, Appli
9	695	97.7	519	2	US-10-295-723-85 Sequence 85, Appli
10	694	97.6	162	2	US-10-282-622-6 Sequence 6, Appli
11	621	87.3	147	2	US-10-282-622-4 Sequence 4, Appli
12	404	56.8	146	2	US-09-522-217-56 Sequence 56, Appli
13	404	56.8	146	2	US-09-923-246-56 Sequence 56, Appli
14	404	56.8	146	2	US-10-295-723-56 Sequence 56, Appli
15	404	56.8	146	2	US-09-825-561A-47 Sequence 47, Appli
16	394	55.4	510	2	US-09-522-217-89 Sequence 89, Appli
17	394	55.4	510	2	US-09-923-246-89 Sequence 89, Appli
18	394	55.4	510	2	US-10-295-723-89 Sequence 89, Appli
19	212	29.8	40	2	US-09-522-217-72 Sequence 72, Appli
20	212	29.8	40	2	US-09-923-246-72 Sequence 72, Appli
21	212	29.8	40	2	US-10-295-723-72 Sequence 72, Appli
22	176	24.8	32	2	US-09-522-217-73 Sequence 73, Appli
23	176	24.8	32	2	US-09-923-246-73 Sequence 73, Appli
24	176	24.8	32	2	US-10-295-723-73 Sequence 73, Appli
25	99.5	14.0	114	1	US-08-031-399-6 Sequence 6, Appli
26	99.5	14.0	114	1	US-08-031-399-12 Sequence 12, Appli

27	99.5	14.0	114	1	US-08-393-305-3 Sequence 3, Appli
28	99.5	14.0	114	1	US-08-726-817-3 Sequence 3, Appli
29	99.5	14.0	114	1	US-08-504-042-6 Sequence 6, Appli
30	99.5	14.0	114	1	US-08-504-042-12 Sequence 12, Appli
31	99.5	14.0	114	1	US-08-725-969-3 Sequence 3, Appli
32	99.5	14.0	114	1	US-08-794-524-3 Sequence 3, Appli
33	99.5	14.0	114	2	US-09-189-193-3 Sequence 3, Appli
34	99.5	14.0	114	2	US-09-462-941-20 Sequence 20, Appli
35	99.5	14.0	114	5	PCT-US94-03793-6 Sequence 6, Appli
36	99.5	14.0	114	5	PCT-US94-03793-12 Sequence 12, Appli
37	99.5	14.0	162	1	US-08-031-399-5 Sequence 5, Appli
38	99.5	14.0	162	1	US-08-393-305-2 Sequence 2, Appli
39	99.5	14.0	162	1	US-08-535-733-2 Sequence 2, Appli
40	99.5	14.0	162	1	US-08-726-817-2 Sequence 2, Appli
41	99.5	14.0	162	1	US-08-504-042-5 Sequence 5, Appli
42	99.5	14.0	162	1	US-08-725-969-2 Sequence 2, Appli
43	99.5	14.0	162	2	US-08-794-524-2 Sequence 2, Appli
44	99.5	14.0	162	2	US-08-842-947-6 Sequence 6, Appli
45	99.5	14.0	162	2	US-09-189-193-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-522-217-2
Sequence 2, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Preenell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: PatSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-522-217-2

Query Match 99.3%; Score 706; DB 2; Length 162;

Best local similarity 100.0%; Pred. No. 5.4e-73;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 2 OGGDRHMRQLDIDVQKNYNDVPELPAPDEVNTNCEWSAFSPKAKLTKANT 61

Db 30 OGGDRHMRQLDIDVQKNYNDVPELPAPDEVNTNCEWSAFSPKAKLTKANT 89

Query 62 GNNRIINVSIIKLLKRPSTNAGRRKRLTSCPSDYKKPKFLEKFKSLLOQMIH 121

Db 90 GNNRIINVSIIKLLKRPSTNAGRRKRLTSCPSDYKKPKFLEKFKSLLOQMIH 149

Query 122 QHLSRTGSEDS 134

Db 150 QHLSRTGSEDS 162

```
RESULT 2
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foeter, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

Query Match          99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  QGODRHIMIRKQLIDIVDQKKNYNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 61
Db      30  QGODRHIMIRKQLIDIVDQKKNYNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 89
Qy      62  GNNERIINVSICKLKRRPSTNAGROKRLTCPSCDSEYKKPKPEFLERFKSLIQMIH 121
Db      90  GNNERIINVSICKLKRRPSTNAGROKRLTCPSCDSEYKKPKPEFLERFKSLIQMIH 149
Qy      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162

RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foeter, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
```

```
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2

Query Match          99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  QGODRHIMIRKQLIDIVDQKKNYNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 61
Db      30  QGODRHIMIRKQLIDIVDQKKNYNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 89
Qy      62  GNNERIINVSICKLKRRPSTNAGROKRLTCPSCDSEYKKPKPEFLERFKSLIQMIH 121
Db      90  GNNERIINVSICKLKRRPSTNAGROKRLTCPSCDSEYKKPKPEFLERFKSLIQMIH 149
Qy      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162

RESULT 4
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match          99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  QGODRHIMIRKQLIDIVDQKKNYNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 61
Db      30  QGODRHIMIRKQLIDIVDQKKNYNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 89
Qy      62  GNNERIINVSICKLKRRPSTNAGROKRLTCPSCDSEYKKPKPEFLERFKSLIQMIH 121
Db      90  GNNERIINVSICKLKRRPSTNAGROKRLTCPSCDSEYKKPKPEFLERFKSLIQMIH 149
Qy      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162
```

RESULT 5
US-10-282-622-2
Sequence 2, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-622-2

Query Match 99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRQLIDIVDQKNYNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
DB 30 QGDRHMRQLIDIVDQKNYNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
QY 62 GNNRIINVSICKLKRKPPSTNAGRQKRLTSCSCSYEKKPKFELERFKSLQKMIH 121
DB 90 GNNRIINVSICKLKRKPPSTNAGRQKRLTSCSCSYEKKPKFELERFKSLQKMIH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162

RESULT 6
US-09-949-016-10307
Sequence 10307, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10307
LENGTH: 174
TYPE: PRT
ORGANISM: Human
US-09-949-016-10307

Query Match 99.3%; Score 706; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 6e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRQLIDIVDQKNYNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
DB 42 QGDRHMRQLIDIVDQKNYNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 101

QY 62 GNNRIINVSICKLKRKPPSTNAGRQKRLTSCSCSYEKKPKFELERFKSLQKMIH 121
DB 102 GNNRIINVSICKLKRKPPSTNAGRQKRLTSCSCSYEKKPKFELERFKSLQKMIH 161
QY 122 QHLSRTHGSEDS 134
DB 162 QHLSRTHGSEDS 174

RESULT 7
US-09-522-217-85
Sequence 85, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-522-217-85

Query Match 97.7%; Score 695; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDRHMRQLIDIVDQKNYNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANTGN 63
DB 389 QDRHMRQLIDIVDQKNYNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANTGN 448
QY 64 NERIINVSICKLKRKPPSTNAGRQKRLTSCSCSYEKKPKFELERFKSLQKMIH 123
DB 449 NERIINVSICKLKRKPPSTNAGRQKRLTSCSCSYEKKPKFELERFKSLQKMIH 508
QY 124 LSSRTHGSEDS 134
DB 509 LSSRTHGSEDS 519

RESULT 8
US-09-923-246-85
Sequence 85, Application US/09923246
Patent No. 6605272
GENERAL INFORMATION:
APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MBP-human zalpha1 ligand fusion polypeptide
US-09-923-246-85

Query Match 97.7%; Score 695; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ODRHMIRROLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 63
Db 389 ODRHMIRROLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 448
Qy 64 NERIINVSICKLKKRPSTNAGRQKRLTCPCSDSYEKKPKPEFLERFKSLQKMIH 123
Db 449 NERIINVSICKLKKRPSTNAGRQKRLTCPCSDSYEKKPKPEFLERFKSLQKMIH 508
Qy 124 LSSRTHGSEDS 134
Db 509 LSSRTHGSEDS 519

RESULT 9
US-10-295-723-85
Sequence 85, Application US/10295723
Patent No. 6686178
GENERAL INFORMATION:
APPLICANT: No. 6686178a, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: MBP-human zalpha1 ligand fusion polypeptide
US-10-295-723-85
Query Match 97.7%; Score 695; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ODRHMIRROLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 63
Db 389 ODRHMIRROLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 448
Qy 64 NERIINVSICKLKKRPSTNAGRQKRLTCPCSDSYEKKPKPEFLERFKSLQKMIH 123
Db 449 NERIINVSICKLKKRPSTNAGRQKRLTCPCSDSYEKKPKPEFLERFKSLQKMIH 508
Qy 124 LSSRTHGSEDS 134
Db 509 LSSRTHGSEDS 519

RESULT 10
US-10-282-622-6
Sequence 6, Application US/10282622
Patent No. 692932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 692932a, Julia E.
TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 162
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalpha1 ligand Q153D/I156D
US-10-282-622-6

Query Match 97.6%; Score 694; DB 2; Length 162;
Best Local Similarity 98.5%; Pred. No. 1.3e-71;
Matches 131; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QGODRMIRROLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANT 61
Db 30 QGODRMIRROLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANT 89
Qy 62 GNERIINVSICKLKKRPSTNAGRQKRLTCPCSDSYEKKPKPEFLERFKSLQKMIH 121
Db 90 GNERIINVSICKLKKRPSTNAGRQKRLTCPCSDSYEKKPKPEFLERFKSLQKMIH 149
Qy 122 QHLSRTHGSEDS 134
Db 150 QHLSRTHGSEDS 162

RESULT 11
US-10-282-622-4
Sequence 4, Application US/10282622
Patent No. 692932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 692932a, Julia E.
TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622

```
/ CURRENT FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: 60/337,586
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 147
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: zalphall ligand Q153ST/1156D
US-10-282-622-4

Query Match      87.3%; Score 621; DB 2; Length 147;
Best Local Similarity 99.2%; Pred. No. 2,7e-63;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGODRHMRQILIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSANT 61
DB 30 QGODRHMRQILIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSANT 89
62 GNNRRIINVSIKKLRKRPSTNAGRQKHRLTCSYCKKPKPELERSKSLQKMH 119
DB 90 GNNRRIINVSIKKLRKRPSTNAGRQKHRLTCSYCKKPKPELERSKSLQKMH 147

RESULT 12
US-09-522-217-56
/ Sequence 56, Application US/09522217
/ Patent No. 6307024
/ GENERAL INFORMATION:
/ APPLICANT: No. 6307024ak, Julia E.
/ APPLICANT: Prensell, Scott R.
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Foster, Donald C.
/ APPLICANT: Holly, Richard D.
/ APPLICANT: Gross, Jane A.
/ APPLICANT: Johnston, Janet V.
/ APPLICANT: Nelson, Andrew J.
/ APPLICANT: Dillon, Stacey R.
/ APPLICANT: Hammond, Angela K.
/ TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
/ FILE REFERENCE: 99-16
/ CURRENT APPLICATION NUMBER: US/09/522,217
/ EARLIER FILING DATE: 2000-03-09
/ EARLIER APPLICATION NUMBER: US 60/123,547
/ EARLIER FILING DATE: 1999-03-09
/ EARLIER APPLICATION NUMBER: US 60/123,904
/ EARLIER FILING DATE: 1999-03-11
/ EARLIER APPLICATION NUMBER: US 60/142,013
/ EARLIER FILING DATE: 1999-07-01
/ NUMBER OF SEQ ID NOS: 115
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 56
/ LENGTH: 146
/ TYPE: PRF
/ ORGANISM: mus musculus
US-09-522-217-56

Query Match      56.8%; Score 404; DB 2; Length 146;
Best Local Similarity 62.1%; Pred. No. 2e-38;
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
```

```
DB 143 QHLS 146

RESULT 13
US-09-923-246-56
/ Sequence 56, Application US/09923246
/ Patent No. 6605272
/ GENERAL INFORMATION:
/ APPLICANT: No. 6605272ak, Julia E.
/ APPLICANT: Prensell, Scott R.
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Foster, Donald C.
/ APPLICANT: Holly, Richard D.
/ APPLICANT: Gross, Jane A.
/ APPLICANT: Johnston, Janet V.
/ APPLICANT: Nelson, Andrew J.
/ APPLICANT: Dillon, Stacey R.
/ APPLICANT: Hammond, Angela K.
/ TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
/ FILE REFERENCE: 99-16
/ CURRENT APPLICATION NUMBER: US/09/923,246
/ EARLIER FILING DATE: 2001-08-03
/ EARLIER APPLICATION NUMBER: US/09/522,217
/ PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
/ NUMBER OF SEQ ID NOS: 115
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 56
/ LENGTH: 146
/ TYPE: PRF
/ ORGANISM: mus musculus
US-09-923-246-56

Query Match      56.8%; Score 404; DB 2; Length 146;
Best Local Similarity 62.1%; Pred. No. 2e-38;
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 2 QGODRHMRQILIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSANT 61
DB 23 QGPRRLIRLRHLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSANT 82
62 GNNRRIINVSIKKLRKRPSTNAGRQKHRLTCSYCKKPKPELERSKSLQKMH 121
DB 83 GNNRRIINVSIKKLRKRPSTNAGRQKHRLTCSYCKKPKPELERSKSLQKMH 142
QY 122 QHLS 125
DB 143 QHLS 146

RESULT 14
US-10-295-723-56
/ Sequence 56, Application US/10295723
/ Patent No. 6686178
/ GENERAL INFORMATION:
/ APPLICANT: No. 6686178ak, Julia E.
/ APPLICANT: Prensell, Scott R.
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Foster, Donald C.
/ APPLICANT: Holly, Richard D.
/ APPLICANT: Gross, Jane A.
/ APPLICANT: Johnston, Janet V.
/ APPLICANT: Nelson, Andrew J.
/ APPLICANT: Dillon, Stacey R.
/ APPLICANT: Hammond, Angela K.
/ TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
/ FILE REFERENCE: 99-16
/ CURRENT APPLICATION NUMBER: US/10/295,723
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: 09/522,217
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:52:43 ; Search time 180 Seconds
(without alignments)
344.838 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711
Sequence: 1 MCGDRHMRKQLIDVDQ.....LQGMHQLHSRTGSEDS 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptocdata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	99.3	133	5	US-10-867-992-19
2	706	99.3	162	3	US-09-923-246-2
3	706	99.3	162	3	US-09-825-561A-10
4	706	99.3	162	3	US-09-972-218A-19
5	706	99.3	162	4	US-10-264-634-19
6	706	99.3	162	4	US-10-285-723-2
7	706	99.3	162	4	US-10-282-622-2
8	706	99.3	162	4	US-10-456-780-2
9	706	99.3	162	4	US-10-659-684-2
10	706	99.3	162	4	US-10-620-169-2
11	706	99.3	162	5	US-10-872-087-10
12	706	99.3	162	5	US-10-787-442-2
13	706	99.3	162	5	US-10-951-239-2
14	706	99.3	162	5	US-10-775-204-2177
15	706	99.3	162	6	US-11-174-398-2
16	706	99.3	162	6	US-11-134-489-2
17	706	99.3	162	6	US-11-132-947-5
18	706	99.3	162	6	US-11-197-468-19
19	706	99.3	162	6	US-11-197-221-1
20	696	97.9	160	6	US-10-775-204-2167
21	695	97.7	131	5	US-10-867-992-16
22	695	97.7	131	6	US-11-132-947-2
23	695	97.7	519	3	US-09-923-246-85
24	695	97.7	519	4	US-10-295-723-85
25	695	97.7	519	4	US-10-659-684-85
26	695	97.7	519	5	US-10-787-442-85
27	694	97.6	162	4	US-10-282-622-6

28	694	97.6	162	6	US-11-174-398-6	Sequence 6, Appli
29	661	93.0	133	5	US-10-867-992-12	Sequence 12, Appli
30	656	92.3	133	5	US-10-867-992-14	Sequence 14, Appli
31	650	91.4	131	5	US-10-867-992-10	Sequence 10, Appli
32	645	90.7	131	5	US-10-867-992-4	Sequence 4, Appli
33	645	90.7	131	5	US-10-867-992-6	Sequence 6, Appli
34	644	90.6	131	5	US-10-867-992-8	Sequence 8, Appli
35	642	90.3	131	5	US-10-867-992-2	Sequence 2, Appli
36	621	87.3	147	4	US-10-282-622-4	Sequence 4, Appli
37	621	87.3	147	6	US-11-174-398-4	Sequence 4, Appli
38	535	75.2	152	6	US-11-132-947-12	Sequence 12, Appli
39	404	56.8	146	3	US-09-923-246-56	Sequence 56, Appli
40	404	56.8	146	3	US-09-825-561A-47	Sequence 47, Appli
41	404	56.8	146	4	US-10-295-723-56	Sequence 56, Appli
42	404	56.8	146	4	US-10-456-780-4	Sequence 4, Appli
43	404	56.8	146	4	US-10-659-684-56	Sequence 56, Appli
44	404	56.8	146	4	US-10-872-087-47	Sequence 47, Appli
45	404	56.8	146	5	US-10-787-442-56	Sequence 56, Appli

ALIGNMENTS

```

RESULT 1
US-10-867-992-19
; Sequence 19, Application US/10867992
; Publication No. US20050124044A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqian; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: US 60/427,772
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO. 19
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-867-992-19

Query Match      99.3%; Score 706; DB 5; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  QGDRHMRKQLIDVDQLNKYNVDLVPFRLPAPEDVETNCMSAFSCFOKAOLKSANT 61
        |||||
DB      1  QGDRHMRKQLIDVDQLNKYNVDLVPFRLPAPEDVETNCMSAFSCFOKAOLKSANT 60

QY      62 GNNRIINVSITKIKRRPSTNAGRRORHRTCPSCSYEKKPPEFIERKSLQKMIH 121
        |||||
DB      61 GNNRIINVSITKIKRRPSTNAGRRORHRTCPSCSYEKKPPEFIERKSLQKMIH 120

QY      122 QHLSRTGSEDS 134
        |||||
DB      121 QHLSRTGSEDS 133

RESULT 2
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia B.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Grose, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.

```

APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-2

Query Match 99.3%; Score 706; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHIMRKQOLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSAANT 61
30 QGODRHIMRKQOLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSAANT 89
QY 62 GNNERIINVSICKLKRKPSTNAGRRQKHRLTCPSCSYKPKPEFLERFKSLLQKMIH 121
90 GNNERIINVSICKLKRKPSTNAGRRQKHRLTCPSCSYKPKPEFLERFKSLLQKMIH 149
QY 122 QHLSRTHGSEDS 134
150 QHLSRTHGSEDS 162
DB

RESULT 3

US-09-825-561A-10
Sequence 10; Application US/09825561A
Patent No. US20020137677A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. US20020137677A1ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match 99.3%; Score 706; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHIMRKQOLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSAANT 61
30 QGODRHIMRKQOLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSAANT 89
QY 62 GNNERIINVSICKLKRKPSTNAGRRQKHRLTCPSCSYKPKPEFLERFKSLLQKMIH 121

|||||
DB 90 GNNERIINVSICKLKRKPSTNAGRRQKHRLTCPSCSYKPKPEFLERFKSLLQKMIH 149
QY 122 QHLSRTHGSEDS 134
150 QHLSRTHGSEDS 162
DB

RESULT 4

US-09-972-218A-19
Sequence 19; Application US/09972218A
Publication No. US20030049798A1
GENERAL INFORMATION:
APPLICANT: Carter, Laura
APPLICANT: White, Matthew J
APPLICANT: Collins, Mary
APPLICANT: Young, Deborah A.
APPLICANT: Donaldson, Debra D.
APPLICANT: Lowe, Leslie D.
APPLICANT: Unger, Michelle
TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
FILE REFERENCE: 22058-552CIP2
CURRENT APPLICATION NUMBER: US/09/972,218A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/569384
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/560766
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US/6057128
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 162
TYPE: PRT
ORGANISM: Human
US-09-972-218A-19

Query Match 99.3%; Score 706; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHIMRKQOLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSAANT 61
30 QGODRHIMRKQOLIDIVDQKNVNDLVPEFLPAPEDEVETNCESAFSCFOKAOLKSAANT 89
QY 62 GNNERIINVSICKLKRKPSTNAGRRQKHRLTCPSCSYKPKPEFLERFKSLLQKMIH 121
90 GNNERIINVSICKLKRKPSTNAGRRQKHRLTCPSCSYKPKPEFLERFKSLLQKMIH 149
QY 122 QHLSRTHGSEDS 134
150 QHLSRTHGSEDS 162
DB

RESULT 5

US-10-264-634-19
Sequence 19; Application US/10264634
Publication No. US20030108549A1
GENERAL INFORMATION:
APPLICANT: Donaldson, Debra et al.
TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor Ac
FILE REFERENCE: G15320-P3
CURRENT APPLICATION NUMBER: US/10/264,634
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 09/040,005
PRIOR FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: 09/560,766
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/569,384
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/972,218
PRIOR FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/373,746
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 162
TYPE: PRT
ORGANISM: Human
US-10-264-634-19

Query Match 99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 61
DB 30 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 89
DB 90 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162

RESULT 6

US-10-295-723-2
Sequence 2, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: No. US20030125524A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-723-2

Query Match 99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 61
DB 30 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 89
QY 62 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 121
DB 90 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 149

QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162

RESULT 7

US-10-282-622-2
Sequence 2, Application US/10282622
Publication No. US20030134390A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. US20030134390A1ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-622-2

Query Match 99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 61
DB 30 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 89
QY 62 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 121
DB 90 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162

RESULT 8

US-10-456-780-2
Sequence 2, Application US/10456780
Publication No. US20040009150A1
GENERAL INFORMATION:
APPLICANT: Nelson, Andrew J.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
OTHER THERAPEUTIC APPLICATIONS
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-456-780-2

Query Match 99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 61
DB 30 QGODRHMIIRKQLIDIVDQKNYNDLVPEPLPAPEDEVETNCESAFSCFOKAOLKSANT 89
QY 62 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 121
DB 90 GNNERIINVSIIKDKRRKPPSTNAGRQKHRLTSPSCSYEKKPPKEFLERFKSLLQKMIH 149

Db 30 QGQDRMRMRQLIDVLDPQLKNYVNDLVPEFLPAPBDVETNCMSAFSCFQKALMSANT 89

Qy 62 GNNERLIINSIKKLKRKPPSTNAGRQKRLTCPSCDSYEKKPKPEFLERFKSLQRMH 121

Db 90 GNNERLIINSIKKLKRKPPSTNAGRQKRLTCPSCDSYEKKPKPEFLERFKSLQRMH 149

Qy 122 QHLSRTHGSEDS 134

Db 150 QHLSRTHGSEDS 162

RESULT 9
US-10-659-684-2
; Sequence 2, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:

```
?
? APPLICANT: Novak, Julia E.
? APPLICANT: Preenell, Scott R.
? APPLICANT: Sprecher, Cindy A.
? APPLICANT: Foster, Donald C.
? APPLICANT: Holly, Richard D.
? APPLICANT: Gross, Jane A.
? APPLICANT: Johnston, Janet V.
? APPLICANT: Nelson, Andrew J.
? APPLICANT: Dillon, Tracey R.
? APPLICANT: Hammond, Angela K.
? TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAN1 LIGAND
? FILE REFERENCE: 99-16
? CURRENT APPLICATION NUMBER: US/10/659,684
? CURRENT FILING DATE: 2003-09-10
? PRIOR APPLICATION NUMBER: US/09/522,217
? PRIOR FILING DATE: 2000-03-09
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
? NUMBER OF SEQ ID NOS: 115
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO: 2
? LENGTH: 162
? TYPE: prt
? ORGANISM: Homo sapiens
?-S-10-659-684-2
```

Query Match	99.3%	Score 706	DB 4	Length 162
Best Local Similarity	100.0%	Pred. No. 4.7e-67		
Matches 133	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	2	QCGDRHIMRQRLIDVQLKNYVNDLPEFLPAEDVETNCMSAFSCFOKALKSANT	61	
Db	30	QCGDRHIMRQRLIDVQLKNYVNDLPEFLPAEDVETNCMSAFSCFOKALKSANT	89	
Qy	62	GNNERIINVISIKLKRKPSTNAGRQKRLTCPCSDSYEKKPKFLEPKFSILQMTIH	121	
Db	90	GNNERIINVISIKLKRKPSTNAGRQKRLTCPCSDSYEKKPKFLEPKFSILQMTIH	149	
Qy	122	QHLSTRHGSSEDS	134	
Db	150	QHLSTRHGSSEDS	162	

RESULT 10
US-10-620-169-2
; Sequence 2, Application US/10620169
: Publication No. US20040136954A1

APPLICANT: Grusby, Michael J
APPLICANT: Wurster, Andrea
APPLICANT: Young, Deborah
APPLICANT: Collins, Mary

```

APPLICANT: Whitters, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
TITLE OR INVENTION: Cell Development and Function
FILE REFERENCE: 22058-585
CURRENT APPLICATION NUMBER: US/10/620,169
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,160
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/403,001
PRIOR FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-620-169-2

Query Match          99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

[illegible]

```

RESULT 11
US-10-872-087-10
/ Sequence 10, Application US/10872087
/ Publication No. US20040235743A1
/ GENERAL INFORMATION:
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Novak, Julia E.
/ APPLICANT: West, James W.
/ APPLICANT: Holly, Richard D.
/ APPLICANT: Nelson, Andrew J.
/ TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOXINE RECEPTORS
/ FILE REFERENCE: 00-22D1
/ CURRENT APPLICATION NUMBER: US/10/872,087
/ CURRENT FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: US 60/194,731
/ PRIOR FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: US 60/222,121
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 09/825,561
/ PRIOR FILING DATE: 2001-04-03
/ NUMBER OF SEQ ID NOS: 86
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10
/ LENGTH: 162
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-872-087-10

```

```

Query Match:      99.3%; Score 706; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 4,7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 30 QGQDHRMIRKRLDIYVQLNYYNDLVPELPAPEDEVENCEMSASCCQKQKLSANT 89
62 GNNERIINVSIKLKRKPEPTNAGRKOKRLTCPSCDSEYKKPEFLERFKSLQRMIH 121
|||||


```
Db      30  QGQDRHMRQQLIDIVDQKNYVNDLVPEFLPAPEDEVETNCENSAPSCFOKAQLKSANT 89
QY      62  GNNERIINVSIIKKLKRKPPSTNAGRQKRLTCSYEEKPPKEFLERFKSLIQMIH 121
Db      90  GNNERIINVSIIKKLKRKPPSTNAGRQKRLTCSYEEKPPKEFLERFKSLIQMIH 149
QY      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162
```

RESULT 15

```
US-11-174-398-2
; Sequence 2, Application US/11174398
; Publication No. US20050244930A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: Novak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/11/174,398
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/282,622
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-398-2
```

```
Query Match      99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2  QGQDRHMRQQLIDIVDQKNYVNDLVPEFLPAPEDEVETNCENSAPSCFOKAQLKSANT 61
Db      30  QGQDRHMRQQLIDIVDQKNYVNDLVPEFLPAPEDEVETNCENSAPSCFOKAQLKSANT 89
QY      62  GNNERIINVSIIKKLKRKPPSTNAGRQKRLTCSYEEKPPKEFLERFKSLIQMIH 121
Db      90  GNNERIINVSIIKKLKRKPPSTNAGRQKRLTCSYEEKPPKEFLERFKSLIQMIH 149
QY      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162
```

Search completed: August 14, 2006, 21:56:26
Job time : 180 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:53:33 ; Search time 33 Seconds

(without alignment)
273.328 Million cell updates/sec

Title: US-10-735-149-28
Sequence: 1 MCGQDRMIRMRLIDVDQ.....LQKMIHQHLSRTHGSEDS 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US09_NEW_PUB pep.*
2: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US06_NEW_PUB pep.*
3: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US07_NEW_PUB pep.*
4: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US08_NEW_PUB pep.*
5: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/PCT_NEW_PUB pep.*
6: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US10_NEW_PUB pep.*
7: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US11_NEW_PUB pep.*
8: /EMC_Ceitera_SIDS3/pcodara/1/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	134	6 US-10-735-149-28	Sequence 28, Appl
2	706	99.3	162	6 US-10-511-937-2572	Sequence 2572, Ap
3	706	99.3	162	6 US-10-735-149-2	Sequence 10, Appl
4	706	99.3	162	6 US-10-806-611-10	Sequence 2, Appl
5	695	97.7	131	6 US-10-806-611-2	Sequence 2, Appl
6	524	73.7	122	6 US-10-806-611-12	Sequence 12, Appl
7	404	56.8	146	6 US-10-806-611-13	Sequence 13, Appl
8	394	55.4	122	6 US-10-806-611-4	Sequence 4, Appl
9	99.5	14.0	162	6 US-10-511-937-2499	Sequence 2499, Ap
10	74.5	10.5	431	7 US-11-056-355B-36356	Sequence 36356, A
11	74.5	10.5	431	7 US-11-056-355B-45283	Sequence 45283, A
12	74.5	10.5	441	7 US-11-056-355B-36355	Sequence 36355, A
13	74.5	10.5	441	7 US-11-056-355B-45282	Sequence 45282, A
14	74.5	10.5	463	7 US-11-056-355B-36354	Sequence 36354, A
15	74.5	10.5	463	7 US-11-056-355B-45281	Sequence 45281, A
16	71	10.0	555	7 US-11-056-355B-79971	Sequence 79971, A
17	71	10.0	631	7 US-11-056-355B-79970	Sequence 79970, A
18	71	10.0	864	7 US-11-056-355B-79969	Sequence 79969, A
19	70.5	9.9	352	7 US-11-056-355B-81843	Sequence 81843, A
20	70.5	9.9	565	6 US-10-471-571A-5038	Sequence 5038, Ap
21	70	9.8	861	6 US-10-520-470-73	Sequence 73, Appl
22	69.5	9.8	720	6 US-10-449-902-51542	Sequence 51542, A
23	69.5	9.8	864	7 US-11-251-208-77	Sequence 77, Appl
24	69	9.7	707	7 US-11-293-697-3241	Sequence 3241, Ap
25	68.5	9.6	212	7 US-11-056-355B-4865	Sequence 4865, Ap

26	68.5	9.6	247	7 US-11-056-355B-56995	Sequence 56995, A
27	68.5	9.6	335	7 US-11-056-355B-4864	Sequence 4864, Ap
28	68.5	9.6	417	7 US-11-056-355B-4863	Sequence 4863, Ap
29	68	9.6	320	7 US-11-056-355B-41014	Sequence 41014, A
30	68	9.6	328	7 US-11-056-355B-41013	Sequence 41013, A
31	68	9.6	1166	6 US-10-449-902-37528	Sequence 37528, A
32	67.5	9.5	378	6 US-10-953-349-32621	Sequence 32621, A
33	67.5	9.5	378	6 US-11-056-355B-64212	Sequence 64212, A
34	67.5	9.5	436	6 US-10-953-349-32620	Sequence 32620, A
35	67.5	9.5	436	6 US-11-056-355B-64211	Sequence 64211, A
36	67.5	9.5	461	6 US-10-953-349-32619	Sequence 32619, A
37	67.5	9.5	461	6 US-11-056-355B-64210	Sequence 64210, A
38	67.5	9.5	763	6 US-10-449-902-33868	Sequence 33868, A
39	67	9.4	179	6 US-10-449-902-49207	Sequence 49207, A
40	67	9.4	299	7 US-11-056-355B-20307	Sequence 20307, A
41	67	9.4	323	6 US-10-449-902-39494	Sequence 39494, A
42	67	9.4	617	7 US-11-056-355B-46959	Sequence 46959, A
43	67	9.4	619	7 US-11-056-355B-46958	Sequence 46958, A
44	66.5	9.4	171	6 US-10-953-349-16629	Sequence 16629, A
45	66	9.3	227	6 US-10-953-349-27717	Sequence 27717, A

ALIGNMENTS

```

RESULT 1
US-10-735-149-28
Sequence 28, Application US/10735149
Publication No. US20060134754A1
GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 134
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Optimized IL-21
US-10-735-149-28

Query Match      100.0%; Score 711; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3e-62;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MCGQDRMIRMRLIDVDQKRYVNDLVPKLPAPADVTNCEWSAFSCFOXAQLSAN 60
DB      1 MCGQDRMIRMRLIDVDQKRYVNDLVPKLPAPADVTNCEWSAFSCFOXAQLSAN 60
QY      61 TGNRRIRINYSIKGLKKPKPSTNAGROKRLTSCPSDSEYKPKPKFLSRFKSLQKMI 120
DB      61 TGNRRIRINYSIKGLKKPKPSTNAGROKRLTSCPSDSEYKPKPKFLSRFKSLQKMI 120
QY      121 HOHLISRTGSEDS 134
DB      121 HOHLISRTGSEDS 134

RESULT 2
US-10-511-937-2572
Sequence 2572, Application US/10511937
Publication No. US2006008836A1

```

```

: GENERAL INFORMATION:
: APPLICANT: EXPRESSION DIAGNOSTICS, INC.
: APPLICANT: Wohlgenuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Woodward, Robert
: APPLICANT: Ly, Ngoc
: APPLICANT: Prentice, James
: APPLICANT: Morris, Macdonald
: APPLICANT: Rosenberg, Steven
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
: TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
: FILE REFERENCE: 506612000104
: CURRENT APPLICATION NUMBER: US/10/511,937
: CURRENT FILING DATE: 2004-10-19
: PRIOR APPLICATION NUMBER: PCT/US2003/012946
: PRIOR FILING DATE: 2003-04-24
: PRIOR APPLICATION NUMBER: US 10/131,831
: PRIOR FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: US 10/325,899
: PRIOR FILING DATE: 2002-12-20
: NUMBER OF SEQ ID NOS: 3117
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 2572
: LENGTH: 162
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-511-937-2572
```

```

Query Match          99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,1e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
        |||
DB      30  QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
        |||
QY      62  GNNERIINVSIKKLRKRPSTNAGRRQKRLTCPCSDSYEKKPPKEFLERFKSLLOQMIIH 121
        |||
DB      90  GNNERIINVSIKKLRKRPSTNAGRRQKRLTCPCSDSYEKKPPKEFLERFKSLLOQMIIH 149
        |||
QY      122 QHLSRTHGSEDS 134
        |||
DB      150 QHLSRTHGSEDS 162
        |||
```

```

RESULT 3
US-10-735-149-2
: Sequence 2, Application US/10735149
: Publication No. US20060134754A1
: GENERAL INFORMATION:
: APPLICANT: Chan, Chung
: APPLICANT: Zamost, Bruce L.
: APPLICANT: Covert, Douglas C.
: APPLICANT: Liu, Hong Y.
: APPLICANT: De Jongh, Karen S.
: APPLICANT: Meyer, Jeffrey D.
: APPLICANT: Holderman, Susan D.
: TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
: TITLE OF INVENTION: IN A PROKARYOTIC HOST
: FILE REFERENCE: 02-12
: CURRENT APPLICATION NUMBER: US/10/735,149
: CURRENT FILING DATE: 2003-12-12
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 162
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-735-149-2
```

```

Query Match          99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,1e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2  QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
        |||
DB      30  QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
        |||
QY      62  GNNERIINVSIKKLRKRPSTNAGRRQKRLTCPCSDSYEKKPPKEFLERFKSLLOQMIIH 121
        |||
DB      90  GNNERIINVSIKKLRKRPSTNAGRRQKRLTCPCSDSYEKKPPKEFLERFKSLLOQMIIH 149
        |||
QY      122 QHLSRTHGSEDS 134
        |||
DB      150 QHLSRTHGSEDS 162
        |||
```

```

RESULT 4
US-10-806-611-10
: Sequence 10, Application US/10806611
: Publication No. US20060159655A1
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Chin, Elaine Y.
: APPLICANT: Senices, Mayra
: APPLICANT: Young, Deborah A.
: TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
: TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
: FILE REFERENCE: 16158-013001
: CURRENT APPLICATION NUMBER: US/10/806,611
: CURRENT FILING DATE: 2004-03-22
: PRIOR APPLICATION NUMBER: US 60/456,920
: PRIOR FILING DATE: 2003-03-21
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 10
: LENGTH: 162
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-806-611-10
```

```

Query Match          99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,1e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
        |||
DB      30  QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
        |||
QY      62  GNNERIINVSIKKLRKRPSTNAGRRQKRLTCPCSDSYEKKPPKEFLERFKSLLOQMIIH 121
        |||
DB      90  GNNERIINVSIKKLRKRPSTNAGRRQKRLTCPCSDSYEKKPPKEFLERFKSLLOQMIIH 149
        |||
QY      122 QHLSRTHGSEDS 134
        |||
DB      150 QHLSRTHGSEDS 162
        |||
```

```

RESULT 5
US-10-806-611-2
: Sequence 2, Application US/10806611
: Publication No. US20060159655A1
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Chin, Elaine Y.
: APPLICANT: Senices, Mayra
: APPLICANT: Young, Deborah A.
: TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
: TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
: FILE REFERENCE: 16158-013001
: CURRENT APPLICATION NUMBER: US/10/806,611
: CURRENT FILING DATE: 2004-03-22
: PRIOR APPLICATION NUMBER: US 60/456,920
: PRIOR FILING DATE: 2003-03-21
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.2
```


SEQ ID NO 2
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
US-10-806-611-2

Query Match 97.7%; Score 635; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 1e-60;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 63
DB 1 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 60
QY 64 NERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 123
DB 61 NERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 120
QY 124 LSSRTGSEDS 134
DB 121 LSSRTGSEDS 131

RESULT 6

US-10-806-611-12
Sequence 12, Application US/10806611
Publication No. US20060159655A1

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806, 611
PRIOR FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456, 920
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 122
TYPE: PRT
ORGANISM: Bos taurus
US-10-806-611-12

Query Match 73.7%; Score 524; DB 6; Length 122;
Best Local Similarity 80.3%; Pred. No. 4.6e-44;
Matches 98; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 4 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 63
DB 1 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 60
QY 64 NERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 123
DB 61 NERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 120
QY 124 LS 125
DB 121 LS 122

US-10-806-611-13
Sequence 13, Application US/10806611
Publication No. US20060159655A1

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.

TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806, 611
PRIOR FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456, 920
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-13

Query Match 56.8%; Score 404; DB 6; Length 146;
Best Local Similarity 62.1%; Pred. No. 2.9e-32;
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 2 QGDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANT 61
DB 23 QGDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANT 82
QY 62 GNERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 121
DB 83 GNERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 142
QY 122 QHLS 125
DB 143 QHLS 146

RESULT 8

US-10-806-611-4
Sequence 4, Application US/10806611
Publication No. US20060159655A1

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806, 611
PRIOR FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456, 920
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 122
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-4

Query Match 55.4%; Score 394; DB 6; Length 122;
Best Local Similarity 62.0%; Pred. No. 2.2e-31;
Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 5 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 64
DB 2 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 61
QY 65 ERIINVSIKKLKKRPSTNAGRQKHRLTGPCSDSYEKKEPKFLEKFKSLQKMIHQH 124
DB 62 KTFIIRIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 121
QY 125 S 125
DB 122 S 122

```

RESULT 9
US-10-511-937-2499
; Sequence 2499, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2499
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2499

Query Match          14.0%; Score 99.5; DB 6; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.017;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 15 IDIVDLKNTYNDLVPEF-----LPAPEDVETNCMSAFSCF-----QKQOLKSAKNTGNNE 65
Db 51 VNYSIDKK-IEDLIQSMHIDATLYTESDVHPSCKVAMKCFLELQVISLESQDASIH 109
QY 66 RIINVSIKKLKRPSTNAGRRQKRLTCPSCDSEYKKPKPEFLERFKSLLOQMTH 121
Db 110 TWENLIT--LANNLSNNGVNTS--GCKECELKEKNITKPELQSFVHIVQMFIN 160

RESULT 10
US-11-056-355B-36356
; Sequence 36356, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36356
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(431)
; OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-36356

Query Match          10.5%; Score 74.5; DB 7; Length 431;
Best Local Similarity 21.8%; Pred. No. 15;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

```

```

QY 6 RHMIRMQQLIDIVDLKNTYNDLVPEFLPAPEDVETNCMSAFSCFQKQOLKSAKNTGNNE 65
Db 220 KYKLARKFLVDVPELGNSTYNEVI-----APDIATYGGICALASFRRSLK-----Q 267
QY 66 RIINVSIKKLKRPSTNAGRRQKRLTCPSCDSEYKKPKPEFLERFKSLLOQMTH 123
Db 268 KVIDININFRNLELVDVRELINDFYSSRYASC-----LEYLASKSNLLDIDLHL 318

RESULT 11
US-11-056-355B-45283
; Sequence 45283, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 45283
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(431)
; OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-45283

Query Match          10.5%; Score 74.5; DB 7; Length 431;
Best Local Similarity 21.8%; Pred. No. 15;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 6 RHMIRMQQLIDIVDLKNTYNDLVPEFLPAPEDVETNCMSAFSCFQKQOLKSAKNTGNNE 65
Db 220 KYKLARKFLVDVPELGNSTYNEVI-----APDIATYGGICALASFRRSLK-----Q 267
QY 66 RIINVSIKKLKRPSTNAGRRQKRLTCPSCDSEYKKPKPEFLERFKSLLOQMTH 123
Db 268 KVIDININFRNLELVDVRELINDFYSSRYASC-----LEYLASKSNLLDIDLHL 318

RESULT 12
US-11-056-355B-36355
; Sequence 36355, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36355
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(441)
; OTHER INFORMATION: Ceres Seq. ID no. 13575997
US-11-056-355B-36355

```

```

; OTHER INFORMATION: Ceres Seq. ID no. 13575996
US-11-056-355B-36354

Query Match      10.5%; Score 74.5; DB 7; Length 463;
Best Local Similarity 21.8%; Pred. No. 16;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY RHMIRMQLDIYDOLKNVYNDLVPEFLPAPDEVETNCESAFSCFOKAOLKSANTGNNE 65
Db KYTLAAKRPDLVPNELGNSYNEVI-----APODATYGICALASFPRSELK-----Q 299
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 66 RI-I-NVSIKKLAKRKPSTNAGRRQKHRLTCPSCDSYEKKPKPFLEFRKSLIQMIHQH 123
Db KYIDNIINFRNFLVLVPVRELINDPYSSRYASC-----LEYIASLKSNLLLDIHILH 350
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 15
US-11-056-355B-45281
; Sequence 45281, Application US/11056355B
; Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Broeyer, Vyacheslav
TITLE OR INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590P052
CURRENT APPLICATION NUMBER: US/11/056,355B
PRIOR FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ. ID NOS: 119966
SEQ ID NO 45281
LENGTH: 463
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1) : (463)
OTHER INFORMATION: Ceres Seq. ID no. 13575996
US-11-056-355B-45281

Query Match      10.5%; Score 74.5; DB 7; Length 463;
Best Local Similarity 21.8%; Pred. No. 16;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY RHMIRMQLDIYDOLKNVYNDLVPEFLPAPDEVETNCESAFSCFOKAOLKSANTGNNE 65
Db KYTLAAKRPDLVPNELGNSYNEVI-----APODATYGICALASFPRSELK-----Q 299
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 66 RI-I-NVSIKKLAKRKPSTNAGRRQKHRLTCPSCDSYEKKPKPFLEFRKSLIQMIHQH 123
Db KYIDNIINFRNFLVLVPVRELINDPYSSRYASC-----LEYIASLKSNLLLDIHILH 350
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Search completed: August 14, 2006, 21:57:05
Job time : 34 secs

```

THIS PAGE LEFT BLANK

CC described above; (2) producing IL-21 proteins; (3) isolating insoluble IL-21 protein; and (4) a composition comprising an IL-21 protein comprising amino acids; residues of the 134 amino acid sequence given in SEQ ID NO:28 (ADP70485) at a concentration of about 10 mg/ml IL-21 protein in 10 mM histidine, and 4.7 % mannitol at pH 5.3. The composition and methods are useful for the large-scale production of IL-21 in prokaryotic hosts. The CC present sequence represents a human IL-21 protein which has been codon optimized for prokaryotic expression, which is used in an example from the present invention.

XX
CC
XX
SQ Sequence 134 AA;

Query Match 100.0%; Score 711; DB 8; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.le-73;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSAN 60
DB 1 MOGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSAN 60
QY 61 TGNERRIIVNSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 120
DB 61 TGNERRIIVNSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 120
QY 121 HOHLSSRTHGSEDS 134
DB 121 HOHLSSRTHGSEDS 134

QY 121 HOHLSSRTHGSEDS 134
DB 121 HOHLSSRTHGSEDS 134

RESULT 2
ID ADW43687 standard; protein; 133 AA.
XX
AC ADW43687;

XX
DT 24-MAR-2005 (first entry)

XX
DE Mature human interleukin-21.

XX
KW Interleukin-21; Antiallergic; Antiasthmatic; Antiparasitic;
KW Antinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;
KW Immune disorder; asthma; parasitic infection; inflammation;
KW multiple sclerosis; cancer; neoplasm; infection.

XX
OS Homo sapiens.

XX
PN WO2004112703-A2.

XX
PD 29-DEC-2004.

XX
PF 15-JUN-2004; 2004WO-US018903.

XX
PR 19-JUN-2003; 2003US-0479772P.

XX
PA (CENZ) CENTOCOR INC.

XX
PI Cunningham MR, Heaven GA, Luo J, Song XR;

XX
DR WPI; 2005-048751/05.

XX
DR N-PSDB; ADW43686.

PT New polynucleotides encoding interleukin-21 analogs, useful for treating
PT allergic diseases as well as asthma, parasitic diseases, inflammatory
PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.

XX
PS Claim 4; SEQ ID NO 19; 28pp; English.

CC The invention relates to an isolated polynucleotides encoding interleukin-21 analogs. Also included are the interleukin-21 analog proteins, a vector comprising the polynucleotide, an isolated host cell comprising the vector and a process for producing a polypeptide comprising culturing the host cell under conditions for production of the polypeptide. The CC polynucleotides and polypeptides, composition and method are useful for

CC treating allergic diseases as well as asthma, parasitic diseases,
CC inflammatory diseases such as multiple sclerosis, cancer, or infectious
CC diseases. The present sequence represents the wild-type mature human IL-21.

XX
SQ Sequence 133 AA;

Query Match 99.3%; Score 706; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 OGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSANT 61
DB 1 OGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSANT 60
QY 62 GNNERRIIVNSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 121
DB 61 GNNERRIIVNSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 120
QY 122 OHLSSRTHGSEDS 134
DB 121 OHLSSRTHGSEDS 133

RESULT 3
ID AAB18623 standard; protein; 162 AA.
XX
AC AAB18623;

XX
DT 22-JAN-2001 (first entry)

XX
DE A human zalphal1 ligand polypeptide.

XX
KW zalphal1 ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX
OS Homo sapiens.

XX
PN WO200053761-A2.

XX
PD 14-SEP-2000.

XX
PF 09-MAR-2000; 2000WO-US006067.

XX
PR 09-MAR-1999; 99US-00264908.

XX
PR 11-MAR-1999; 99US-00265992.

XX
PR 01-JUL-1999; 99US-0142013P.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

XX
DR Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX
DR N-PSDB; AAA75552.

PT New human cytokine, designated zalphal1 ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.

XX
PS Disclosure; Page 205-206; 256pp; English.

CC The present sequence represents a human zalphal1 ligand polypeptide, which is a cytokine. The zalphal1 ligand is useful for stimulating the proliferation and development of haematopoietic cells in vitro and in vivo. Zalphal1 ligand polynucleotides can be used as primers or probes for cloning the zalphal1 gene. The zalphal1 ligand is useful for treating tumorigenesis. A zalphal1 ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphal1 ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in

CC regulating hematopoiesis. The zalphall ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphall ligand
CC genetic defect

XX Sequence 162 AA;

Query Match 99.3%; Score 706; DB 3; Length 162;

Best Local Similarity 100.0%; Pred. No. 5.2e-73; Indels 0; Gaps 0;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QGDRHMRMQLIDIVQLKNVNDLVEFLPAPEDVETNCESAFSCFOKAQKSNANT 61
DB 30 QGDRHMRMQLIDIVQLKNVNDLVEFLPAPEDVETNCESAFSCFOKAQKSNANT 89
OY 62 GNNERRIIVSIKIKLRKPPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121
DB 90 GNNERRIIVSIKIKLRKPPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149
OY 122 QHLSRRTGSEDS 134
DB 150 QHLSRRTGSEDS 162

RESULT 4

AAE13729
ID AAE13729 standard; protein; 162 AA.

AC AAE13729;

DT 26-FEB-2002 (first entry)

DE Human soluble Zalphall cytokine receptor ligand protein.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
XX inflammatory disorder; haemostatic; cell proliferation; immune disorder;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
XX ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
XX viral infection.

OS Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..31

XX Protein /label= Signal_peptide

XX Region /label= Mature_zalphall_ligand

XX Region /label= Helix_A

XX Region /label= Helix_B

XX Region /label= Helix_C

XX Region /label= Helix_D

XX Region /note= "Conserved region"

XX MO200177171-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-US010872.

XX 05-APR-2000; 2000US-0194731P.

XX 28-JUL-2000; 2000US-0222121P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX WPI; 2002-025898/03.
DR N-PSDB; AAD22923.

XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
PT antagonist for stimulating ligand activity-induced proliferation of
PT hematopoietic cells and for suppressing immune response in a mammal.

XX Claim 1; Page 181; 243pp; English.

XX The invention relates to an isolated soluble zalphall cytokine receptor
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for
CC inhibiting or antagonizing the ligand activity-induced proliferation of
CC haematopoietic cells and haematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalpha is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is human soluble zalphall cytokine receptor ligand

SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 5; Length 162;

Best Local Similarity 100.0%; Pred. No. 5.2e-73; Indels 0; Gaps 0;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QGDRHMRMQLIDIVQLKNVNDLVEFLPAPEDVETNCESAFSCFOKAQKSNANT 61
DB 30 QGDRHMRMQLIDIVQLKNVNDLVEFLPAPEDVETNCESAFSCFOKAQKSNANT 89
OY 62 GNNERRIIVSIKIKLRKPPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121
DB 90 GNNERRIIVSIKIKLRKPPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149
OY 122 QHLSRRTGSEDS 134
DB 150 QHLSRRTGSEDS 162

RESULT 5

AAU1965
ID AAU1965 standard; protein; 162 AA.

AC AAU1965;

DT 09-APR-2002 (first entry)

DE Human zalphall ligand polypeptide.

XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
XX B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human; hPBCS;
XX activated human peripheral blood cell.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..31

XX Protein /label= Signal_peptide

XX /label= Mature_zalphall_ligand

XX US6307024-B1.

XX 23-OCT-2001.

XX 09-MAR-2000; 2000US-00522217.

XX 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Novak JB, Presnell SR, Sprecher CA, Foster DC, Holly RD,
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
DR WPI; 2002-040208/05.
DR N-PSDB; AAS20637.
XX
PT New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX Claim 7; Col 125-126; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall ligand gene,
CC and in gene therapy. Zalphall ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC human zalphall ligand polypeptide. The cDNA encoding this is isolated
CC from a cDNA library from activated human peripheral blood cells (hPBcs)
XX
XX Sequence 162 AA;
XX
XX Query Match 99.3%; Score 706; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QGODRHMRKQLDIYDQKYNVNDLVPEFLPAPEDEVETNCESAFSCFOKQLKSANT 61
DB 30 QGODRHMRKQLDIYDQKYNVNDLVPEFLPAPEDEVETNCESAFSCFOKQLKSANT 89
QY 62 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121
DB 90 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162
XX
XX RESULT 6
ABR61407
ID ABR61407 standard; protein; 162 AA.
XX
XX ABR61407;
AC
XX
XX 12-AUG-2003 (first entry)
DT
XX
XX Human IL-21 SEQ ID NO:19.
DE
XX
XX arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
KW immune cell activity; cancer; infectious disorder; antineumatic;
KW antiarthritic; osteopathic; antiparasitic; cytosolic; antibacterial;
KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
KW neuroprotective; antitumor; antiallergic; antianemic; hepatotropic;
KW antithyroid; antiinflammatory; immune response; immune disorder;

KW autoimmune disease; human.
XX
XX Homo sapiens.
OS
XX
XX WO2003028630-A2.
XX
XX
XX 10-APR-2003.
XX
XX 04-OCT-2002; 2002WO-US029839.
XX
XX
XX 04-OCT-2001; 2001US-00972218.
PR 17-APR-2002; 2002US-0373746P.
XX
XX
XX (AMHP) WYETH.
PA
PI Carter L, Whiters MJ, Collins M, Young DA, Larsen G,
PI Donaldson DD, Lowe JD, Dunne K, Ma M, Witke JS, Kasasian MT;
PI Ungar M;
XX
XX WPI; 2003-430146/40.
DR
DR N-PSDB; ACC80873.
XX
XX
XX Treating or preventing arthritic disorder, cancer or infectious disorders
PT in a subject, involves administering a modulator of interleukin-21 or its
PT receptor which modulate immune cell activity.
XX
XX Disclosure; Page 37; 176pp; English.
XX
XX The invention relates to a novel method for treating or preventing an
CC arthritic disorder in a subject. The method involves administering to the
CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
CC optionally in combination with another therapeutic agent, to inhibit or
CC reduce immune cell activity in the subject. The method is also useful for
CC treating or preventing cancer or an infectious disorder, in a subject, by
CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
CC method of the invention has antirheumatic, antiarthritic, osteopathic,
CC antiparasitic, cytosolic, antibacterial, virucide, antiparasitic,
CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
CC antitumor, antiallergic, antianemic, hepatotropic,
CC antithyroid, and antiinflammatory activity. The method is useful for
CC treating or preventing an arthritic disorder such as rheumatoid
CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
CC arthritis or ankylosing spondylitis, and also cancer such as solid
CC tumour, soft tissue tumour or metastatic lesion, or an infectious
CC disorder such as a bacterial, viral or parasitic infection in a mammal,
CC preferably human. A method of the invention is also useful for
CC increasing the ability of a vaccine composition containing an antigen to
CC elicit a protective immune response in a subject against the antigens.
CC The antigen is from a pathogen such as virus, bacterium or protozoan, or
CC from cancer or tumour cell antigen, or expressed on the surface of cancer
CC cell. An alternative method of the invention is useful for modulating the
CC activity of immune or haematopoietic cells and thus to treat or prevent a
CC variety of immune disorders, such as autoimmune diseases, for example
CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
CC The present sequence is used in an exemplification of the invention
XX
XX Sequence 162 AA;
XX
XX Query Match 99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QGODRHMRKQLDIYDQKYNVNDLVPEFLPAPEDEVETNCESAFSCFOKQLKSANT 61
DB 30 QGODRHMRKQLDIYDQKYNVNDLVPEFLPAPEDEVETNCESAFSCFOKQLKSANT 89
QY 62 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121
DB 90 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149
QY 122 QHLSRTHGSEDS 134

Db 150 QHLSRTHGSEDS 162

|||||

RESULT 7

AAE14932

ID AAE14932 standard; protein; 162 AA.

XX AAE14932;

XX AC AAE14932;

XX DT 27-AUG-2003 (first entry)

XX DE Human interleukin-21 (IL-21).

XX KM Interleukin-21; IL-21; antagonist; cancer; inflammatory;

XX KM autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

XX KM systemic lupus erythematosus; myasthenia gravis; diabetes; human;

XX KM zalphall ligand.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 41..56

FT Binding-site /label= Helix_A

FT Binding-site 44

FT Binding-site /note= "Important for IL-21 binding to its receptor"

FT Region 57..68

FT Region /label= A/B_loop

FT Region 69..84

FT Region /label= Helix_B

FT Region 85..91

FT Region /label= B/C_loop

FT Region 92..105

FT Region /label= Helix_C

FT Region 106..134

FT Region /label= C/D_loop

FT Region 135..148

FT Binding-site /label= Helix_D

FT Binding-site 135

FT Binding-site /note= "Important for IL-21 binding to its receptor"

PN WO2003040313-A2.

XX 15-MAY-2003.

XX PF 28-OCT-2002; 2002WO-US034502.

XX PR 05-NOV-2001; 2001US-0337586P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, West JW, Novak JE;

XX DR WPI: 2003-441547/41.

XX DR N-PSDB; AAD47852.

XX PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing

XX PT and treating disorders with aberrant expression or activity of the IL-21

XX PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and

XX PT diabetes.

XX PS Disclosure; Page 53-54; 71pp; English.

XX CC The invention relates to polynucleotides and polypeptides of interleukin-

XX CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50

XX CC that is not detectable in receptor binding studies. The antagonists of

XX CC the invention have mutations in the D helix of the IL-21 molecule, and

XX CC can be used to inhibit the activity of IL-21 with its cognate receptor.

XX CC The IL-21 antagonists are useful for diagnosing and treating disorders

XX CC involving the aberrant expression or activity of the IL-21 polypeptide,

XX CC such as cancer, inflammatory and autoimmune disorders, including

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,

CC myasthenia gravis and diabetes. The polypeptides can also be used to

CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,

CC and for enhancing in vivo killing of target tissues. The present sequence

CC is human IL-21 (originally designated zalphall ligand)

XX SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 7; Length 162;

Best Local Similarity 100.0%; Pred. No. 5,2e-73;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMIKRLIDIVDLKNVNDLVEFLPAPEDEVETNCWSAFSCFOKAQLKSANT 61

DB 30 QGDRHMIKRLIDIVDLKNVNDLVEFLPAPEDEVETNCWSAFSCFOKAQLKSANT 89

QY 62 GNNERIINVSIKKIKRRPPTNAGRRQKRLTCSGDSYEKKPFLERKSLIQKMIH 121

DB 90 GNNERIINVSIKKIKRRPPTNAGRRQKRLTCSGDSYEKKPFLERKSLIQKMIH 149

QY 122 QHLSRTHGSEDS 134

DB 150 QHLSRTHGSEDS 162

RESULT 8

ABU62893

ID ABU62893 standard; protein; 162 AA.

XX AC ABU62893;

XX DT 15-SEP-2003 (first entry)

XX DE Human interleukin 21 (IL-21).

XX KM Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;

XX KM cytosolic; antibacterial; virucide; antianaemic; gene therapy;

XX KM haematopoiesis; anaemias; immune response; cancer; infection;

XX KM transplanted organ; cytokine; receptor; interleukin 21; IL21.

XX OS Homo sapiens.

XX PN US2003049798-A1.

XX PD 13-MAR-2003.

XX PF 04-OCT-2001; 2001US-00972218.

XX PR 17-MAR-1998; 98US-00040005.

XX PR 28-APR-2000; 2000US-00560766.

XX PR 11-MAY-2000; 2000US-00569384.

XX PA (CARTER L.

XX PA (WHITT/ WHITTERS M J.

XX PA (COLL/ COLLINS M.

XX PA (YOUNG/ YOUNG D A.

XX PA (DONA/ DONALDSON D D.

XX PA (LOWE/ LOWE L D.

XX PA (UNGE/ UNGER M.

XX PI Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;

XX PI Lowe LD, Unger M;

XX DR WPI: 2003-513354/48.

XX DR N-PSDB; ACD26729.

XX PT New fusion polypeptide for regulating hematopoiesis and immune responses,

XX PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion

XX PT polypeptide.

XX PS Disclosure; Page 10; 26pp; English.

XX CC The invention describes a fusion polypeptide comprising at least a

fragment of a WT-1 polypeptide and a non-WT-1 fusion polypeptide. The
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
CC anaemias) and/or immune responses (e.g. immune response to cancer,
CC infections or to a transplanted organ) and in identifying other members
CC of the haematopoietin superfamily, including cytokines and receptors. The
CC polynucleotide may be used to express recombinant protein for analysis,
CC characterisation or therapeutic use; and as markers for tissues or
CC chromosomes. The polypeptide and polynucleotide may also be used as
CC nutritional sources or supplements. This is the amino acid sequence of
CC human interleukin 21 (IL21), a cytokine receptor that can be used to
CC characterise the novel haematopoietin receptor of the invention
SQ Sequence 162 AA;
QY Query Match 99.3%; Score 706; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2 QGODRHMIRKQLIDIVDQKNVNDLVPEFLPAPEDEVETNCMSAFSCFOKQOLKSANT 61
30 QGODRHMIRKQLIDIVDQKNVNDLVPEFLPAPEDEVETNCMSAFSCFOKQOLKSANT 89
QY 62 GNNERRIINVSIKKLRKRPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQRMH 121
DB 90 GNNERRIINVSIKKLRKRPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQRMH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162
RESULT 9
ADE85808 ID ADE85808 standard; protein; 162 AA.
XX ADE85808;
XX 29-JAN-2004 (first entry)
XX Human interleukin-21.
XX Human; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;
KW antiinflammatory; dermatological; ophthalmological; uropathic;
KW muscular-gen.; vasotrophic; antidiabetic; antihypoid; thyromimetic;
KW neuroprotective; gastrointestinal-gen.; antiporiatic; gene therapy.
XX Homo sapiens.
OS WO2003087320-A2.
XX 23-OCT-2003.
XX 08-APR-2003; 2003WO-US010736.
XX 09-APR-2002; 2002US-0371038P.
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX MOLL T, Strom TB, Zheng XX;
XX WPI; 2003-845317/78.
XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,
PT treating and prognosticating autoimmune disorders, e.g. rheumatic
PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis
PT and myasthenia gravis.
XX Disclosure; SEQ ID NO 1; 65pp; English.
XX The present sequence is the protein sequence of human interleukin-21 (IL-
CC 21). The invention provides antagonists of the IL-21 receptor. These
CC include mutants of murine IL-21 in which the Gln residue at position 119
CQ of the mature polypeptide is substituted by Asp or in which the Gln

residues at positions 114 and 119 of the mature polypeptide are both
CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell
CC activation. They preferably comprise a sequence that increases
CC circulating half-life, such as the FC region of an IgG molecule and may
CC further comprise an antigenic tag. Such antagonists inhibit cellular
CC proliferation in response to either anti-CD3 monoclonal antibodies or
CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with
CC IL-21. A claimed method of suppressing the immune response in a patient
CC comprises administering the IL-21 antagonist or a nucleic acid encoding
CC it. The method is used to treat an autoimmune disease such as rheumatic
CC disease, including systemic lupus erythematosus, Sjogren's syndrome,
CC scleroderma, mixed connective tissue disease, dermatomyositis,
CC polymyositis, Reiter's syndrome, or Bence's disease, or rheumatoid
CC arthritis, type I diabetes, autoimmune disease of the thyroid such as
CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the
CC central nervous system such as multiple sclerosis, myasthenia gravis, or
CC cephalalomyelitis, or an autoimmune disease selected from pemphigus
CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome,
CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all
CC claimed).
SQ Sequence 162 AA;
QY Query Match 99.3%; Score 706; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 2 QGODRHMIRKQLIDIVDQKNVNDLVPEFLPAPEDEVETNCMSAFSCFOKQOLKSANT 61
30 QGODRHMIRKQLIDIVDQKNVNDLVPEFLPAPEDEVETNCMSAFSCFOKQOLKSANT 89
QY 62 GNNERRIINVSIKKLRKRPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQRMH 121
DB 90 GNNERRIINVSIKKLRKRPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQRMH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162
RESULT 10
ADP17046 ID ADP17046 standard; protein; 162 AA.
XX ADP17046;
XX 12-FEB-2004 (first entry)
XX Human albumin fusion protein-related protein SeqID2177.
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX Homo sapiens.
OS WO2003060071-A2.
XX 24-JUL-2003.
XX 23-DEC-2002; 2002WO-US040891.
XX 21-DEC-2001; 2001US-0341811P.
XX 24-JAN-2002; 2002US-0350358P.
XX 26-FEB-2002; 2002US-0351360P.
XX 26-FEB-2002; 2002US-0359370P.
XX 28-FEB-2002; 2002US-0360000P.
XX 27-MAR-2002; 2002US-0367500P.
XX 08-APR-2002; 2002US-0370227P.
XX 10-MAY-2002; 2002US-0378950P.
XX 24-MAY-2002; 2002US-0382617P.
XX 28-MAY-2002; 2002US-0383123P.
XX 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (DELTA) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPAL PHARM CORP.
 XX
 PI Balance DJ, Turner AJ, Rosen CA, Haseltine WA;
 DR WPI; 2003-598517/56.
 DR N-PSDB; ADF17040.
 XX
 PT New albumin fusion protein, useful for preparing a composition for
 treating diabetes mellitus.
 XX
 PS Example 4; SEQ ID NO 2177; 24DP; English.
 XX
 CC This invention relates to a novel albumin fusion protein having albumin
 or biological activity. Human serum albumin is responsible for a
 significant proportion of the osmotic pressure of serum and also
 functions as a carrier of endogenous and exogenous ligands. The fusion of
 albumin to a therapeutic protein may increase shelf-life and stability of
 the therapeutic protein. The albumin fusion protein of the invention may
 allow production of compositions with antidiabetic activity whilst the
 nucleotide sequence which encodes it may be useful for gene therapy. The
 albumin fusion protein is useful for preparing a composition for treating
 diabetes mellitus. The present sequence is that of a therapeutic protein
 which was fused with human albumin to create a novel albumin fusion
 protein of the invention. Note: The sequence data for this patent did not
 form part of the printed specification, but was obtained in electronic
 format directly from WIPO at ftp.wipo.int/pub/publishedpat_sequences
 XX
 SQ Sequence 162 AA;
 Query Match 99.3%; Score 706; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 5,2e-73;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QGQDRHMRKQRLIDIVQLKYNVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 61
 DB 30 QGQDRHMRKQRLIDIVQLKYNVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 89
 QY 62 GNNRRINVSJKLKRKPPSTNAGRQKRLTCSQSYEKKPKPEFLERKSLQKKI 121
 DB 90 GNNRRINVSJKLKRKPPSTNAGRQKRLTCSQSYEKKPKPEFLERKSLQKKI 149
 QY 122 QHLSRTGSEDS 134
 DB 150 QHLSRTGSEDS 162
 RESULT 11
 ADH44572
 ID ADH44572 standard; protein; 162 AA.
 AC ADH44572;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human zalphall ligand protein.
 XX
 KW Human; Zalphall ligand; Zalphall receptor; immune response;
 tumour progression; metastasis; tumour stasis; haematopoietic tumour;
 lymphoma; B cell tumour; systemic lupus erythematosus;
 rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;

KW Immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT 1..31
 FT /note="Signal peptide"
 FT Protein 32..162
 FT /note="Mature zalphall, claimed in claim 1"
 XX
 FN US6605272-B2.
 XX
 PD 12-AUG-2003.
 XX
 PF 03-AUG-2001; 2001US-00923246.
 XX
 PR 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 PR 09-MAR-2000; 2000US-00522217.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 DR WPI; 2003-895283/82.
 XX
 CC Stimulating an immune response in a mammal exposed to an antigen or
 pathogen, useful for enhancing anti-tumor activity resulting in reduced
 tumor progression or metastasis, comprises administering zalphall ligand
 polypeptide.
 PT
 PS Claim 1; SEQ ID NO 2; 103DP; English.
 XX
 CC The invention relates to stimulating an immune response in a mammal
 exposed to an antigen or pathogen comprising administering a composition
 comprising mature zalphall ligand polypeptide comprising residues 32-162
 of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
 immune response in a mammal exposed to an antigen or pathogen
 comprising: (a) determining (in)directly the level of antigen or
 pathogen present in the mammal; (b) administering a composition
 comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)
 determining (in)directly the level of antigen or pathogen in the mammal;
 and (d) comparing the antigen or pathogen level in (a) with (b), where a
 change in the level indicates stimulation of immune response), and
 stimulating an immune response in a mammal exposed to an antigen or
 pathogen comprising: (a) determining a level of antigen- or pathogen-
 specific antibody; (b) administering a composition comprising zalphall
 ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
 administration level of the antigen- or pathogen-specific antibody; and
 (d) comparing the level of the antibody in (a) with (b), where an
 increase in the antibody level indicates stimulation of immune response).
 CC The method is useful for stimulating an immune response in a mammal
 exposed to an antigen or pathogen, and for enhancing anti-tumor activity
 resulting in a reduction in tumour progression, decrease in metastasis,
 or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
 or a B cell tumour. The zalphall ligand is useful for treating a wide
 range of diseases arising from defects in the immune system, e.g.
 systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
 diabetes, for boosting immunity to infectious diseases, treating
 immunocompromised patients, such as HIV+ patients and in improving
 vaccines. The present sequence is a human zalphall ligand protein.
 CC
 XX
 SQ Sequence 162 AA;
 Query Match 99.3%; Score 706; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 5,2e-73;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QGQDRHMRKQRLIDIVQLKYNVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 61
 DB 30 QGQDRHMRKQRLIDIVQLKYNVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 89

```

QY      62 GNNERIINVSIKKLRKRPSTNAGRQKHRLTCPSCSYKKPKFLEERFKSLLOQMIIH 121
      |||
DB      90 GNNERIINVSIKKLRKRPSTNAGRQKHRLTCPSCSYKKPKFLEERFKSLLOQMIIH 149
QY      122 QHLSRTHGSEDS 134
      |||
DB      150 QHLSRTHGSEDS 162

RESULT 12
AD100908
ID      AD100908 standard; protein; 162 AA.
XX
XX      AC      AD100908;
XX
XX      DT      22-APR-2004 (first entry)
XX
DE      Immunity-related human zai1phal1 ligand protein.
XX
KM      zai1phal1 ligand; immunity; infectious disease; immunocompromised patient;
XX      HIV; vaccine; human.
XX
OS      Homo sapiens.
XX
XX      PN      US2003125524-A1.
XX
XX      PD      03-JUL-2003.
XX
XX      PF      15-NOV-2002; 2002US-00295723.
XX
XX      PR      09-MAR-2000; 2000US-00522217.
XX
XX      PA      (Zymo ) ZYMOGENETICS INC.
XX
PI      Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD,
PI      Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
DR      WPI; 2003-811003/76.
DR      N-PSDB; AD100907.
XX
XX      PT      New zai1phal1 ligand polypeptides, useful for boosting immunity to
XX      infectious diseases, and treating immunocompromised patients, such as
XX      human immunodeficiency virus (HIV) patients, or in improving vaccines.
XX
XX      PS      Claim 7; SEQ ID NO 2; 113pp; English.
XX
CC      The invention relates to a novel isolated zai1phal1 ligand polypeptide.
CC      The polypeptide of the invention may be useful for boosting immunity to
CC      infectious diseases and treating immunocompromised patients, such as HIV
CC      patients, as well as in improving vaccines. The current sequence is that
CC      of the human zai1phal1 ligand protein of the invention.
XX
XX      SQ      Sequence 162 AA:

Query Match      99.3%; Score 706; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QGODRHMIRKQOLIDIYDQKKNYNDLVPEFLPAPEDVETNCWSAFSCFOKQOLKSANT 61
      |||
DB      30 QGODRHMIRKQOLIDIYDQKKNYNDLVPEFLPAPEDVETNCWSAFSCFOKQOLKSANT 89
QY      62 GNNERIINVSIKKLRKRPSTNAGRQKHRLTCPSCSYKKPKFLEERFKSLLOQMIIH 121
      |||
DB      90 GNNERIINVSIKKLRKRPSTNAGRQKHRLTCPSCSYKKPKFLEERFKSLLOQMIIH 149
QY      122 QHLSRTHGSEDS 134
      |||
DB      150 QHLSRTHGSEDS 162

RESULT 13

```

```

ADH10501
ID      ADH10501 standard; protein; 162 AA.
XX
XX      AC      ADH10501;
XX
XX      DT      11-MAR-2004 (first entry)
XX
DE      Human interleukin-21 (IL-21) polypeptide.
XX
XX      IL-21; interleukin-21; cytostatic; virucide; antiinflammatory;
XX      hepatotropic; neuroprotective; muscular; respiratory; antiarthritic;
XX      antibacterial; anti-HIV; gene therapy; cancer; human.
XX
XX      OS      Homo sapiens.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      Peptide      32..162
XX      FT      /note="specifically claimed fragment"
XX      FT      Peptide      41..148
XX      FT      /note="specifically claimed fragment"
XX
XX      PN      WO2003103589-A2.
XX
XX      PD      18-DEC-2003.
XX
XX      PF      06-JUN-2003; 2003WO-US017808.
XX
XX      PR      07-JUN-2002; 2002US-0387127P.
XX
XX      PA      (Zymo ) ZYMOGENETICS INC.
XX
PI      Nelson AJ, Hughes SD, Holly RD, Kindsvogel WR;
DR      WPI; 2004-062206/06.
DR      N-PSDB; ADH10500.
XX
XX      PT      Treating Non-Hodgkin's lymphoma, cancer or infection comprises
XX      administering to the subject a polypeptide having a functional activity
XX      of interleukin-21.
XX
XX      PS      Claim 9; SEQ ID NO 2; 154pp; English.
XX
XX      CC      The invention relates to treating Non-Hodgkin's lymphoma, cancer or
XX      infection and involves administering to the subject a polypeptide having
XX      a functional activity of interleukin-21 (IL-21). The methods are useful
XX      for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma,
XX      epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and
XX      colon cancer; viral infection such as AIDS, Hepatitis B or C virus,
XX      gastroenteritis, haemorrhagic diseases, enteritis, cardiac,
XX      encephalitis, paralytic, bronchitis, upper or lower respiratory
XX      disease, respiratory papillomatosis, arthritis, disseminated disease,
XX      meningitis, and mononucleosis; or bacterial infection, such as an
XX      infection by a bacteria selected from chlamydiae, listeriae, helicobacter
XX      pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden
XX      acute respiratory syndrome caused by a coronavirus, Herpes Simplex
XX      viruses, Epstein-Barr virus, Cytomegalovirus, Pox viruses, Papilloma
XX      virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses,
XX      Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses.
XX      The present sequence represents a human IL-21 polypeptide.
XX
XX      SQ      Sequence 162 AA:

Query Match      99.3%; Score 706; DB 8; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QGODRHMIRKQOLIDIYDQKKNYNDLVPEFLPAPEDVETNCWSAFSCFOKQOLKSANT 61
      |||
DB      30 QGODRHMIRKQOLIDIYDQKKNYNDLVPEFLPAPEDVETNCWSAFSCFOKQOLKSANT 89
QY      62 GNNERIINVSIKKLRKRPSTNAGRQKHRLTCPSCSYKKPKFLEERFKSLLOQMIIH 121
      |||
DB      90 GNNERIINVSIKKLRKRPSTNAGRQKHRLTCPSCSYKKPKFLEERFKSLLOQMIIH 149

```


QY	2	QGDPRHMRKQOLIDIVDQKNYNDLVPEFLPAPEDEVETNCESWAPSCFOKAOLKSANT	61
Db	30	QGDPRHMRKQOLIDIVDQKNYNDLVPEFLPAPEDEVETNCESWAPSCFOKAOLKSANT	89
QY	62	GNNRILINVSIXKLLKRRKPPSTNAGRORHLTCPSCDSEKKPPKEPLERFKSLLOKMIH	121
Db	90	GNNRILINVSIXKLLKRRKPPSTNAGRORHLTCPSCDSEKKPPKEPLERFKSLLOKMIH	149
QY	122	QHLSSRTHGSEDS	134
Db	150	QHLSSRTHGSEDS	162

Search completed: August 14, 2006, 21:46:36
Job time : 198 secs

1	94.5	13.3	162	1	A53484	interleukin-15 precursor
2	91.5	12.9	567	2	S29498	lymphocyte antigen
3	82	11.5	607	1	ABX472	gamma albumin precursor
4	79	11.1	206	2	S49882	hypothetical protein
5	78	11.0	741	2	JC7822	isochlorate dehydratase
6	75.5	10.6	336	2	S42632	Fil-A protein precursor
7	74	10.4	440	2	T47906	FUSCA PROTEIN FUS6
8	74	10.4	2197	2	B71600	variant-specific B
9	73.5	10.3	162	2	I49124	interleukin-15 - p
10	73.5	10.3	472	2	I59087	ISG-K54 - human
11	73.5	10.3	868	2	T31527	hypothetical protease
12	73	10.3	304	2	A32108	translation initiator
13	73	10.3	848	2	T00372	hypothetical protease
14	72.5	10.2	309	2	T41889	PE38 orf153 - Bombyx
15	72.5	10.2	674	2	S61181	hypothetical protease
16	72.5	10.2	1101	2	T26919	hypothetical protease
17	72.5	10.2	1206	2	S24407	fornin isoform IV
18	72	10.1	257	2	C69230	conserved hypothetical
19	72	10.1	262	2	F72858	probable methyl transferase
20	72	10.1	262	2	T41813	ACMPV orf69 - Bombyx
21	71.5	10.1	195	2	S42022	ureidoglycolate hydrolase
22	71.5	10.1	741	2	AB8317	isochlorate dehydratase
23	71	10.0	321	2	T46352	hypothetical protease
24	71	10.0	406	2	T28957	hypothetical protease
25	71	10.0	719	2	T27977	lin-15A protein
26	71	10.0	805	2	A46266	aryl hydrocarbon receptor
27	71	10.0	864	2	T08575	protein kinase homolog
28	71	10.0	899	2	B38529	nibk protein - Escherichia coli
29	71	10.0	1231	2	T22382	hypothetical protease

30	71	10.0	2206	2	G71611	hypothetical protein
31	71	10.0	2934	2	T18378	variant-specific s
32	70.5	9.9	352	2	C68294	T24D18.7 protein -
33	70.5	9.9	447	2	S39316	CAB3b protein - hu
34	70.5	9.9	477	2	S21049	calcium channel pr
35	70.5	9.9	482	2	S41211	voltage-dependent
36	70.5	9.9	484	2	S33315	CAB3a protein - hu
37	70.5	9.9	484	2	A46608	voltage-dependent
38	70.5	9.9	565	2	G89878	conserved hypothet
39	70	9.8	403	2	S71356	glucocorticoid-acti
40	70	9.8	405	2	A73383	sensory histidine k
41	70	9.8	425	2	T50355	hypothetical prote
42	70	9.8	1222	2	C88504	protein B0361.3 (1
43	70	9.8	1366	2	B86292	FMN12 protein -
44	69.5	9.8	380	2	T24554	hypothetical prote
45	69.5	9.8	864	2	S60441	hypothetical prote

ALIGNMENTS

```

RESULT 1
A:3484
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53484
R:Grubstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Beeson, J.; Groll, J.G.
Science 264, 965-968, 1994
A:Title: Cloning of a T cell growth factor that interacts with the beta chain of the interleukin-15 precursor
A:Reference number: A53484; MUID:94233380; PMID:8178155
A:Accession: A53484
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Releashes: 1-162 <GR>
A:Cross-references: UNIPROT:E40221; UNIPARC:UPI000003JAC6; GB:U03099; NID:G493521; PIDN:
A>Note: the complete translation is not shown
C:Superfamily: interleukin-15
C:Keywords: growth factor
F:49-162/Product: interleukin-15 #status predicted <MAT>
F:83-133, 90-136/Disulfide bonds: #status predicted

```

Query Match	13.3%	Score 94.5;	DB 1;	Length 162;
Best Local Similarity	25.9%;	Pred. No. 0.11;		
Matches 30; Conservative	23;	Mismatches 48;	Indels 15;	Gaps 5,

D6
QY 15 IDVIDDKRYVNDLVDEF-----LPAPEVEVNCWSAFSCF----QAOLKSNANTGNE 65
::: :::: :|: |:
D5 51 VNVISDPKK-IDDLQSHMIDATILVTSDVPHSPCKVTKAMKFLLLEQLTYSHESGDDTIHD 109

QY 66 RIINVSIKRKRRPSTAGRQRQKRRLCPGDSYEKKRPKEPLERPSYLQXKH 121
::: :::: :|: |:
D6 110 TWENLT--LANNIUSNNTITES---GCKDEBELENKIIEFLQSOPHYIVQMFIN 160

RESULT 2

1 Lymphocyte antigen Ly84 precursor - mouse
N:Alternate names: 38.5K T1 glycoprotein; ST2L protein
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S29498; A3541; S17657; S07054
C:Yanagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tomioka, S.
PEBS Lett. 318, 83-87, 1993
A:Title: Presence of a novel primary response gene ST2L, encoding a product highly similar
A:Reference number: S29498; MUID:93170492; PMID:7916701
A:Accession: S29498
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-567 <YAN>
A:Cross-references: UNIPROT:P14719; UNIPARC:UPI0000023617; EMBL:D13695; NID:g286100; PDB:
Klevenz, R.; Hoffmann, S.; Werenkefoid, A.K.

Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
A;Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to
A;Reference number: A33541; MUID:89345536; PMID:2527364
A;Accession: A33541
A;Molecule type: mRNA
A;Residues: 1-191; 'V', 193-328, 'SKECPSHIA' <KLE>
A;Cross-references: UNIPARC:UPI0000028A98; GB:M24843; NID:g201103; PIDN:AAA40160.1; PID:
R;Tomlinaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
Biochim. Biophys. Acta 1090, 1-8, 1991
A;Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal map
A;Reference number: S17657; MUID:91355215; PMID:1832015
A;Accession: S17657
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-191; 'V', 193-328, 'SKECPSHIA' <TOM>
A;Cross-references: UNIPARC:UPI0000028A98; EMBL:X60184; NID:g54200; PIDN:CAA42742.1; PID:
R;Tomlinaga, S.I.
FEBS Lett. 258, 301-304, 1989
A;Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si
A;Reference number: S07054; MUID:90092495; PMID:2532153
A;Accession: S07054
A;Molecule type: mRNA
A;Residues: 1-328, 'SKECPSHIA' <TO2>
A;Cross-references: UNIPARC:UPI0000003FD2; EMBL:Y07519; NID:g55517; PIDN:CAA68812.1; PID:
A;Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator
C;Genetics:
A;Gene: ST2
A;Map position: 1
A;Intons: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2
C;Superfamily: Interleukin-1 receptor type 1
C;Keywords: glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-337/Product: ST2 protein #status predicted <MAT>
F;60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 12.9%; Score 91.5; DB 2; Length 567;
Best Local Similarity 25.6%; Pred. No. 0.74;
Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;
Db 19 DOLKNYNDLVPEFLPAPDEVETNCWMSAFSCFOKALTKSANTGNERRIINVSIKLKARK 78
76 DRLK-----FLPAPRV-----DSGIYACV-----IRSENL-NKTKGYLVNTIHK---K 113
QY 79 PPESTN-----AGRRQKHRLTSPSCDSYEKKRPKEFLERFKSLQKMIHQH----- 123
Db 114 PPGCNIPDYLYMYSVVRSDSKNFKITCTPTIDLYMTAVVQWPKNCKALQEPFRFRAHRSYLF 173
QY 124 LSSRTGSE 132
Db 174 IDNVTHDE 182
RESULT 3
ABXL72
74K albumin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B41682; S02693; A05288
R;Moskatis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Paetori, R.L.; Schoenberg, D.R.
Mol. Endocrinol. 3, 464-473, 1989
A;Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic ac
e during development.
A;Reference number: A41682; MUID:89313788; PMID:2747653
A;Accession: B41682
A;Molecule type: mRNA
A;Residues: 3-607 <MOS>
R;Schorpp, M.; Doebeiling, U.; Wagner, U.; Ryffel, G.U.
J. Mol. Biol. 199, 83-93, 1988
A;Title: 5'-flanking and 5'-proximal exon regions of the two xenopus albumin genes. Del
A;Reference number: S02692; MUID:88172470; PMID:2451026
A;Accession: S02693
A;Status: not compared with conceptual translation

A;Molecule type: DNA
A;Residues: 1-48 <SCH>
A;Cross-references: UNIPARC:UPI000017441E; EMBL:Z26826
R;Molfe, A.P.; Glover, J.F.; Martin, S.C.; Tennilwood, M.P.R.; Williams, J.L.; Tata, J.J
Eur. J. Biochem. 146, 489-496, 1985
A;Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and deestabilizator
A;Reference number: A05288; MUID:85126974; PMID:3971963
A;Accession: A05288
A;Molecule type: mRNA
A;Residues: 459-502, 'L', 504-557 <WOL>
A;Cross-references: UNIPARC:UPI000017441F; GB:M28276
A;Note: the authors translated the codon TAT for residue 63 as Thr
C;Comment: Serum albumin is synthesized in the liver as prealbumin. It binds copper, i
mones (weak bonds with these hormones promote their transfer across the membranes), thyr
C;Genetics:
A;Intons: 27/1
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-607/Product: 74k serum albumin #status predicted <MAT>
F;32-201/Domain: serum albumin repeat homology <SA1>
F;32-393/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;30/Binding site: copper (His) #status predicted
F;80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,4
F;256/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 11.5%; Score 82; DB 1; Length 607;
Best Local Similarity 24.2%; Pred. No. 6.3;
Matches 38; Conservative 19; Mismatches 50; Indels 50; Gaps 6;
Db 16 DIVDOLKNYNDLVPEF-----LPAPDEVETNCWMSAFSCF-----QKALKSAN 60
72 EINDPAKSCINDTPEDEKRVGTLFPDKLCADPAVGNTVMSKCAKQDPKAAQCKKAAH 131
QY 61 TGNERRI---NVSIKLKARK-----PSTNAGRQKHRLTSPS 96
Db 132 RDHEHTSIKPEPEETCKLKEHPDILLAFIHEARNHPDYLPAYLALTKQYHKLAEHC 191
QY 97 CDSYEKKRPKEFLERFKSLQKMIHQHLSRTGSED 133
Db 192 CEEEDKE--KCFSEKMKQLMK-----QSHSID 217
RESULT 4
S49882
hypothetical protein Y1127c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein Y18277.Ozc
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S49882
R;Hamlyn, N.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: S49882
A;Accession: S49882
A;Molecule type: DNA
A;Residues: 1-206 <HAM>
A;Cross-references: UNIPROT:PA0470; UNIPARC:UPI000013B441; GB:Z47047; EMBL:Z46833; NID:9C
C;Genetics:
A;Gene: MIPS:Y1127C
A;Cross-references: SGD:S0001389
A;Map position: 9L
Query Match 11.1%; Score 79; DB 2; Length 206;
Best Local Similarity 26.1%; Pred. No. 3.9;
Matches 29; Conservative 18; Mismatches 48; Indels 16; Gaps 3;
Db 20 QLKKNYNDLVPEFLPAPDEVETNCWMSAFSCFOKALTKSANTGNERRIINVSIKLKARK 79
12 QATSVANGLSNLILPGVPKIRANNGKTSVNGSKAQLIDRNKKRQVLQQRDYNHKKKCC 71
QY 80 PSTNAGRQKHRLTSPSCDSYEKKRPKEFLERF--KSLQKMIHQHLSRT 128

Db 72 KLVKKKKVKKHKL-----DKKQLAKHGVKK--HQHGGTLT 108

RESULT 5

JC7822 Isocitrate dehydrogenase (NADP) (EC 1.1.1.42), monomeric type - Azotobacter vinelandii

C/Species: Azotobacter vinelandii

C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C/Accession: JC7822; PC7187

R:Shahar, T.; Takada, Y.; Yamaoka, N.; Fukunaga, N.

Biosci. Biotechnol. Biochem. 66, 489-500, 2002

A/Title: Cloning, sequencing, and expression of a gene encoding the monomeric isocitrate

A/Reference number: JC7822; PMID:12005040; PMID:21999801

A/Accession: JC7822

A/Molecule type: DNA

A/Residues: 1-741 <SAH>

A/Cross-references: UNIPROT:P16100, UNIPARC:UPI000012D1CA, DDBJ:D73443

A/Accession: PC7187

A/Molecule type: protein

A/Residues: 2-16 <SA>

A/Cross-references: UNIPARC:UPI000017CDF5

C/Comment: This enzyme that catalyzes the oxidative decarboxylation of isocitrate to alpha-ketoglutarate, a key step in the tricarboxylic acid cycle, is a typical mesophilic, it contributes to the respiratory protection of nit

C/Genetics:

A:Gene: 1cd

C/Superfamily: isocitrate dehydrogenase, monomeric type

C/Keywords: oxidoreductase

Query Match 11.0%; Score 78; DB 2; Length 741;

Best Local Similarity 24.8%; Pred. No. 18;

Matches 26; Conservative 23; Mismatches 34; Indels 22; Gaps 4;

5 DRHMIRKQLIDVDLKNVNDL-----VPEFLPAEDVETNCESAFSCFOKAOLKS 58

Db 77 DANITKLPNLSASVPOKKAALKEIQOGGYKLPD--PEEKPTDEKDVAKRYDKIGSA 133

59 AN-----TGNRRITNVSICKLKKRPSTNAGROKRLTSPSCDS 99

134 VNVVLRGNSDRAPLSVKNYARKHP-----HKGMSADS 169

RESULT 6

Fit-15 protein precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S42632

R:Berger, G.; Reikertorfer, A.; Braedelmann, S.; Graninger, P.; Bueslinger, M.

EMBO J. 13, 1176-1188, 1994

A/Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA isoforms

A/Reference number: S42632; PMID:94178260; PMID:8131748

A/Accession: S42632

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-336

A/Cross-references: UNIPROT:Q62611, UNIPARC:UPI000002AC15, GB:U04319, NID:G488278, PIDN:

C/Superfamily: vaccinia virus B15R protein; immunoglobulin homology

Query Match 10.6%; Score 75.5; DB 2; Length 336;

Best Local Similarity 22.2%; Pred. No. 14;

Matches 30; Conservative 26; Mismatches 42; Indels 37; Gaps 6;

15 IDVDLKNVNDLVP-----EFLPAEDVETNCESAFSCFOKAOLKSAN 60

Db 49 INVENVYSWTNRIIPQKNRIIVSRDRKLPAPKE-----DSGYTCVIRSP-ESIK 102

61 TGNRRITNVSICKLKKRP-----STNAGROKRLTSPSCDSYEKKRPKEFL 110

103 TGS-----LWTVTK--RPNCKIPDYMTSTVDGSDKSKITPTALTATWTAPOVMPK 155

111 RFSLLQKMTIHLS 125

Db 156 NCKALQGPFRPHNS 170

RESULT 7

T47906 FUSCA PROTEIN FUS6 - Arabidopsis thaliana

N/Alternate names: protein T20K12.40

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004

C/Accession: T47906

R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Meyer, K.F.X.; Queti

submitted to the Protein Sequence Database, January 2000

A/Reference number: 224480

A/Accession: T47906

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-440 <DEH>

A/Cross-references: UNIPROT:P45432, UNIPARC:UPI000016DBFF, EMBL:AL137898

A/Experimental source: cultivar Columbia; BAC clone T20K12

C/Genetics:

A:Map position: 3

A:Introns: 130/3; 237/3; 278/1; 304/2; 382/3

A/Note: T20K12.40

C/Superfamily: COP9 signalosome complex subunit 1

Query Match 10.4%; Score 74; DB 2; Length 440;

Best Local Similarity 22.0%; Pred. No. 25;

Matches 26; Conservative 22; Mismatches 50; Indels 20; Gaps 3;

6 RHMIRKQLIDVDLKNVNDLVEFLPAEDVETNCESAFSCFOKAOLKSANTGNE 65

Db 230 KYKLAARKFLVDNELGNSVNEVI-----APQDIATVGGICALASFRSEIKAF----- 278

66 RIINVSICKLKKRPSTNAGROKRLTSPSCDSYEKKRPKEFLERKSLQKMTIH 123

Db 279 -IDNINFRNLELVDPVRELIINDPYSSRYASC-----LEVIASIKSNLLDIIHL 327

RESULT 8

B71600 variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium falciparum)

N/Alternate names: erythrocyte membrane binding protein 1 (EMP1)

C/Species: Plasmodium falciparum

C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C/Accession: B71600

R:Gardner, M.J.; Tettein, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

; Ferreira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;

Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A/Reference number: A71600; PMID:99021743; PMID:9804551

A/Accession: B71600

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-2197 <GAR>

A/Cross-references: UNIPROT:O96296; UNIPARC:UPI00001796B2; GB:AE001434; GB:AE001362; NID:

A/Experimental source: clone 3D7

C/Genetics:

A:Gene: PFB1055c

Query Match 10.4%; Score 74; DB 2; Length 2197;

Best Local Similarity 29.5%; Pred. No. 1.4e+02;

Matches 28; Conservative 16; Mismatches 41; Indels 10; Gaps 4;

21 LKNVNDLVEFLPAEDVETNCESAF--SCFOKAOLKSANTGNRRINVSICKLKK 78

Db 1594 VKSFLFWIRK-IAVVNDONVTKLSFGNSCGCSAISTN-GNEBDAIDCMIKLEKK 1651

79 -----PSTNAGROKRLTSPSCDSYEKKRPK 107

Db 1652 IDECKRFGNSGTCNETHLPDLDVDEDEPLEE 1686

RESULT 9

```

interleukin-15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: I49124
R:Anderson, D.M.; Johnson, L.; Glaccum, M.B.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.
Genomic 25, 701-706, 1995
A>Title: Chromosomal assignment and genomic structure of IL15.
A:Reference number: A56005; MUID:95278940; PMID:7759105
A:Accession: I49124
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-162 <RES>
C:Gene: IL15
C:Superfamily: interleukin-15

Query Match      10.3%; Score 73.5; DB 2; Length 162;
Best Local Similarity 19.8%; Pred. No. 9.9;
Matches 22; Conservative 30; Mismatches 54; Indels 5; Gaps 3;

QY 15 IDI---VDQKNVYNDL-VPEFLPAPDVTNCMSAFSCFOKAQLKSANTGNRRILNV 70
   || : ::::: || : : : : : : : : : : : : : : : : : : : : : : : :
Db 51 IDAVYDEKIESLIQSIIHPTTLTYDSDFPHSCVATMNG-LLEQLVIIHEYSNMTLNE 109
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 TVRNVLVIANSTLSNNRVASGCKCEBELEKTFTFESFIRIVQMFTIN 160
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
ISG-K54 - human
IS9087
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I59087
R:Levy, D.; Larner, A.; Chaudhuri, A.; Babies, L.E.; Darnell, J.E.
Proc. Natl. Acad. Sci. U.S.A. 83, 8923-8933, 1986
A>Title: Interferon-beta-induced transcription: Isolation of an inducible gene and identification of its promoter.
A:Reference number: I59087; MUID:87067427; PMID:3466167
A:Accession: I59087
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-472 <RES>
A:Cross-references: UNIPROT:P09913; UNIPARC:UPI000012D3E4; GB:M14660; NID:g186559; PIDN:A3; Geneticks:
A:Gene: GDB:IFI54; GIOP2; IFI-54
A:Cross-references: GDB:I19959; OMIM:147040
A:Map position: 10q23-10q24
A:Intons: 2/2
C:Superfamily: interferon-induced 56k protein

Query Match      10.3%; Score 73.5; DB 2; Length 472;
Best Local Similarity 26.9%; Pred. No. 30;
Matches 39; Conservative 18; Mismatches 49; Indels 39; Gaps 8;

QY 7 HMIHQRLDIVDQLKNVYNDLVPEFLPAP--EDVEITNCE--WS-----AFSC 50
   || : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 HMGRLLSDVQIVDKVKI-----VCEKFSPIRIESPFLDCEBGWTRLCGGNQNERAKVC 160
   || : : : : : : : : : : : : : : : : : : : : : : : :

QY 51 FOXAQLKSANTGNRRILNVSIKKLKRPSTNA--GRQRHLITPCSCDSEYKKPKPER 108
   || : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 FEKLLEKPPNPBETSGIAIASYRLDMWPSONAIDLRAQAIRL-----NPDNQY 210
   || : : : : : : : : : : : : : : : : : : : : : : : :

QY 109 LERFKSLQKHIOHLSRSHTGSSED 133
   || : : : : : : : : : : : : : : : : : : : : : : : :
Db 211 L--KVALLALKRK--MREGESEE 229
   || : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
T31527
hypothetical protein Y47D3A.14 - Caenorhabditis elegans

```

C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: J31527
R:Matthews, L.
submitted to the EMBL Data Library, October 1999
A:Reference number: 221043
A:Accession: J31527
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-868 <WIL>
A:Cross-references: UNIPROT:Q9NMA8; UNIPARC:UPI0000179F16; EMBL:AL117202; PIDN:CA855073.1
C:Genetics:
A:Gene: CESP:Y47D3A.14
A:Introns: 17/2; 51/3; 102/3; 169/3; 246/1; 287/2; 319/3; 371/3; 395/2; 440/3; 450/3; 495/2

Query Match
Best Local Similarity 10.3%; Score 73.5; DB 2; Length 869;
Matches 19; Conservative 11; Mismatches 30; Indels 5; Gaps 1;

Cy 45 WSABSCFQKALQS-----ANTGNRRIRIVNSIKKLKKRPSTNAGRRQKRLTSPSCDS 99
Db 680 WSRVQAFKKKMKSGGGGTSNDSSEQBSKYLKKLKKRPSDETVIPVHYIVCPLEFS 739
100 YKKP 104
Db 740 HVAIP 744

RESULT 12
A32108
translation initiation factor eIF-2 alpha chain - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein J1429; protein YJR007w
C:Species: *Saccharomyces cerevisiae*
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A32108; S55195; S57022
R:Cigan, A.M.; Pabich, E.K.; Feng, L.; Donahue, T.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 2784-2788, 1989
A:Title: Yeast translation initiation suppressor su12 encodes the alpha-subunit of eukaryotic
A:Reference number: A32108; MUID:89202411; PMID:2649894
A:Accession: A32108
A:Molecule type: DNA
A:Residues: 1-304 <CTG>
A:Cross-references: UNIPROT:P20459; UNIPARC:UPI00000530CA; EMBL:M25552; NID:g341369; PIDN:R1de Haan, M.; Smits, P.H.M.; Grivelli, L.A.
submitted to the EMBL Data Library, May 1995
A:Reference number: S55183
A:Accession: S55195
A:Molecule type: DNA
A:Residues: 1-304 <DEH>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:X87611; NID:g854567; PIDN:CAA60929.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56771
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57022
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; NID:g101531; PIDN:CAA89529.1; PIDN:R1de Haan, M.; Grivelli, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995

Oy 73 KCLRRKPPSTNAGRQKRLTGPCSDSYEK-----KPPKEFLERFKSLIQ 117
 Db 223 VAAFLVLTQALQKQIGQLS--ALEKITVITKYGVGNITMPKAVTATEDALQ 280
 Oy 118 KMIH-QHLSSTHGSSED 133
 Db 281 ALLESKELDNRSDEDD 297

RESULT 13

T00372
 hypothetical protein KIAA0650 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C/Accession: T00372; T12523

R/Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.

DNA Ref. 5, 169-176, 1998

A/Title: Prediction of the coding sequences of unidentified human genes. X. The complete

A/Reference number: Z14142; MUID:98403880; PMID:9734811

A/Accession: T00372

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-848 <ISH>

A/Cross-references: UNIPROT:O75141; UNIPARC:UPI000006CEB7; EMBL:AB014550; NID:G3327113;

A/Experimental source: brain

R/Wambitt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A/Reference number: Z17524

A/Accession: T12523

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122-848 <WAM>

A/Cross-references: UNIPARC:UPI0000072B1E; EMBL:AL080138

A/Experimental source: adult testis; clone DKFZp434K063

C/Genetics:

A/Note: KIAA0650; DKFZp434K063.1

Query Match 10.3%; Score 73; DB 2; Length 848;
 Best Local Similarity 25.5%; Pred. No. 62;
 Matches 27; Conservative 22; Mismatches 47; Indels 10; Gaps 5;
 Oy 31 EPLPAPEDVETNC-EMSAFSCFOQAOLKSANTGNNERIINVSIRKLRKPPSTNAGRQK 89
 Db 66 KFLIPGPGNDLCTWNEPDSFIRVQLIS--GPPAKLLLDWPELKSIVIN-GRDLQ 121
 Oy 90 HRLTGPCSDSYEKPPKEFLERFKSLQKMHQHL--SSRTHGSED 133
 Db 122 NPILVQLCDQMDNPAP--VQHVXISLTAKSNLKLMPNSNOCHKTDE 164

RESULT 14

T41889
 PE38 off153 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C/Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV

A/Variety: isolate T3

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T41889

R/Gomi, S.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999

A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A/Reference number: Z22020; MUID:99281911; PMID:10355780

A/Accession: T41889

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-309 <KAM>

A/Cross-references: UNIPROT:O92504; UNIPARC:UPI00000F20C2; EMBL:L33180; NID:G3745835; PI

C/Genetics:

A/Note: pe38

C/Superfamily: Orgyia pseudotsugata nuclear polyhedrosis virus PE-38 protein

Query Match 10.2%; Score 72.5; DB 2; Length 309;
 Best Local Similarity 23.4%; Pred. No. 24;

Matches 33; Conservative 30; Mismatches 57; Indels 21; Gaps 6;
 Oy 10 RMROLIDIVDQKRYVNDLVEBFLPAPEDVETNC-----EMSAFSCFOQAOLKSAN----- 60
 Db 148 KTOERVAVQGYKQIIKVLQGRSVISYENSNNCDINNENAKIYALELKNENHSDQ 207
 Oy 61 -TGNNERII-----NVSIRKLRKPPSTNAGRQKRLTGPCSDSYEKPPKEFLERFK 113
 Db 208 VTSERNROLIENTRLNBOVQLGRQ-VRTLAPQR---GITVNPQIGRDDRAPAEINERFR 263
 Oy 114 SLQKMIHQ-HLSRTHGSED 133
 Db 264 SLVYSTISELFEINRVHSION 284

RESULT 15

S61181
 hypothetical protein YDR295C - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein D9740.10

C/Species: Saccharomyces cerevisiae

C/Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C/Accession: S61181

R/Ding, H.

submitted to the EMBL Data Library, June 1995

A/Description: The sequence of S. cerevisiae cosmid 9740.

A/Reference number: S61160

A/Accession: S61181

A/Molecule type: DNA

A/Residues: 1-674 <DIN>

A/Cross-references: UNIPROT:Q06629; UNIPARC:UPI00000531D0; EMBL:U28374; NID:G849207; PID:

C/Genetics:

A/Genes: SGD:PI02; MIPS:YDR295C

A/Cross-references: SGD:S0002703

A/Map position: 4R

Query Match 10.2%; Score 72.5; DB 2; Length 674;
 Best Local Similarity 20.0%; Pred. No. 55;
 Matches 30; Conservative 30; Mismatches 55; Indels 35; Gaps 4;
 Oy 1 MCGQDRMIRKROLID-----IVDQKRYVNDLVEBFLPAPEDV 39
 Db 495 LQNKINHLKRNROELNENFNKLPSNTISSENLLEGSAADLQKKEYIDKNATLFNKLKELQ 554
 Oy 40 ETNCEWGAFA-----SCFOQAOLKSANTGNNERIINVSIRKLRKPP-----STNAGRQ 88
 Db 555 QANAKSKNDELRSKTIQISSKAAESAOYIKILQESMKSLENEVNGPLTFKSTESLAKGE 614
 Oy 89 KHRLTGPCSDSYEKPPKEFLERFKSLQK 118
 Db 615 LERL---QNDPQSLKARNKFLKNVITLMNR 641

Search completed: August 14, 2006, 21:52:27
 Job time : 42 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:43:28 ; Search time 301 Seconds

(without alignments)
411.801 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711
Sequence: 1 MQQODHMTMRQLDIVDQ.....LLQKMHQHLSTRTHSEDS 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	706	99.3	155 1 IL21_HUMAN	Q9B642 homo sapien
2	535	75.2	146 1 IL21_BOVIN	Q76153 sus taurin
3	524	73.7	146 1 IL21_PIG	Q76153 sus scrofa
4	513	72.2	146 1 IL21_CANPA	Q9E171 canis famli
5	404	56.8	146 1 IL21_MOUSE	Q9E171 mus musculu
6	404	56.8	146 1 IL21_MOUSE	Q9E171 mus musculu
7	344	48.4	123 1 IL21_PERMA	Q80XG2 peromyscus
8	149.5	21.0	145 2 OS8IT6_CHICK	Q80XG2 gallus gall
9	101.5	14.3	162 1 IL15_FELCA	Q97687 felis silve
10	99.5	14.0	135 2 Q6FGX7_HUMAN	Q6FGX7 homo sapien
11	99.5	14.0	162 1 IL15_HUMAN	Q40933 homo sapien
12	99.5	14.0	162 2 Q49528_HUMAN	Q49528 homo sapien
13	98.5	13.9	162 1 IL15_RABIT	Q3Y5G8 oryctolagus
14	96.5	13.6	162 2 OSW7F5_BRARE	Q5W7F5 brachydanio
15	94.5	13.3	160 2 Q32PM5_BRARE	Q32PM5 brachydanio
16	94.5	13.3	162 1 IL15_CERAE	Q40221 ceropithec
17	94.5	13.3	162 1 IL15_MACMU	Q40221 macaca mula
18	94.5	13.2	162 2 Q4U0U2_MACTH	Q4U0U2 macaca thib
19	93.5	13.2	162 2 Q381U1_TETNG	Q381U1 tetradodon r
20	92	12.9	163 2 Q2PUG6_RABIT	Q2PUG6 oryctolagus
21	91.5	12.9	337 2 OS0D95_MOUSE	Q5D095 mus musculu
22	91.5	12.9	567 1 IL1L1_MOUSE	Q47719 mus musculu
23	91.5	12.9	567 1 Q3UMS3_MOUSE	Q3UMS3 mus musculu
24	90.5	12.7	162 1 IL15_BOVIN	Q28028 bos taurin
25	89.5	12.6	162 1 IL15_SHEEP	Q28028 bos taurin
26	89.5	12.6	162 2 Q5S529_CAVPO	Q5S529 capra porce
27	87.5	12.3	162 2 Q6B416_MORSE	Q6B416 equus cabal
28	85.5	12.0	105 2 Q5W7F6_BRARE	Q5W7F6 brachydanio
29	85.5	12.0	162 2 Q4GZ11_BUBBU	Q4GZ11 brachydanio
30	85	12.0	162 2 Q5E8K6_MARMO	Q5E8K6 marmota mon
31	85	12.0	162 2 Q5WQV8_MARMO	Q5WQV8 marmota mon

32	84.5	11.9	511 2 Q5A2U1_CANAL	Q5A2U1 candida alb
33	83.5	11.7	466 2 Q5C0J3_SCHJA	Q5C0J3 schistosoma
34	83.5	11.7	582 2 Q8DJ56_SYNEL	Q8DJ56 synecococc
35	83.5	11.7	3052 2 Q82933_9PORT	Q82933 johnsongras
36	83	11.7	607 2 Q642P7_XENLA	Q642P7 xenopus lae
37	82.5	11.6	149 2 Q59A52_FUGRU	Q59A52 figu rubrip
38	82	11.5	607 1 ALBUD_XENLA	ALBUD xenopus lae
39	81.5	11.5	566 2 Q9VYE8_DROME	Q9VYE8 drosophila
40	81	11.4	163 2 Q966R0_DICDI	Q966R0 dictyosteli
41	81	11.4	414 2 Q7MNL4_VIBVY	Q7MNL4 vibrio vuln
42	81	11.4	1111 2 Q6FKH1_CANCA	Q6FKH1 candida gla
43	80.5	11.3	155 2 Q59902_FUGRU	Q59902 figu rubrip
44	80.5	11.3	162 1 IL15_PIG	Q95253 sus scrofa
45	80.5	11.3	353 2 Q2UGB6_ASFOR	Q2UGB6 aspergillus

ALIGNMENTS

RESULT 1
ID IL21_HUMAN STANDARD; PRT: 155 AA.
AC Q9HBE4;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 23-NOV-2004, sequence version 2.
DT 07-FEB-2006, entry version 24.
DE Interleukin-21 precursor (IL-21) (Zell).
GN Name:IL21;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
RA Parikh-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Knipper J.L., Kramer J., Conklin D., Pressnell S.R., Berry J., Shiota F., Bort S., Hanly K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D., "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.", Nature 408:57-63 (2000).
[2]
RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P., Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Mitrak L.A., Nickerson D.A., "SeattleSNPs: NHLBI H66682 program for genomic applications, UW-FORC, Seattle, WA (URL: http://pga.gs.washington.edu).", submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubenberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Shat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marishta K., Farmer A.A., Rubin G.M., Hong L., Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C., Bock S.S., Loquellano N.A., Peters G.J., Abramson J.S., Mullaly S.J., Richards S., Worley K.C., Hais S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting J.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP FUNCTION: Pubmed=15178704; DOI=10.1189/jlb.1003488;
 RX Serengeti M., Julkunen I., Matikainen S.;
 RT "IFN-alpha regulates IL-21 and IL-21R expression in human NK and T
 RT cells."; J. Leukoc. Biol. 76:416-422(2004).
 RN [5]
 RP Pubmed=15147560; DOI=10.1111/j.1365-2567.2004.01886.x;
 RX Sivakumar P.V., Foster D.C., Clegg C.H.;
 RA "Interleukin-21 is a T-helper cytokine that regulates humoral immunity
 RT and cell-mediated anti-tumour response."; Immunology 112:177-182(2004).
 RL -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC production of IgG(1) and IgG(3) in B-cells (By similarity). May
 CC play a role in proliferation and maturation of natural killer (NK)
 CC cells in synergy with IL15. May regulate proliferation of mature
 CC B- and T-cells in response to activating stimuli. In synergy with
 CC IL15 and IL18 stimulates interferon gamma production in T-cells
 CC and NK cells. During T-cell mediated immune response may inhibit
 CC dendritic cells (DC) activation and maturation.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed in activated CD4-positive T-cells
 CC but not in CD8-positive T-cells, B-cells, or monocytes.
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: AF254069; AAC29348.1; ALT_INIT; mRNA.
 CC EMBL: AY763518; AA088182.1; ALT_INIT; Genomic_DNA.
 CC EMBL: BC066258; AA06258.1; ALT_INIT; mRNA.
 CC EMBL: BC066259; AA06259.1; ALT_INIT; mRNA.
 CC EMBL: BC066260; AA06260.1; ALT_INIT; mRNA.
 CC EMBL: BC066261; AA06261.1; ALT_INIT; mRNA.
 CC EMBL: BC066262; AA06262.1; ALT_INIT; mRNA.
 CC EMBL: BC069124; AA069124.1; ALT_INIT; mRNA.
 CC EMBL: ENSG00000138684; Homo sapiens.
 CC HGNC: HGNC:6005; IL21.
 CC MIM: 605384; gene.
 CC DR GO: GO:0005615; C:extracellular space; NAS.
 CC DR GO: GO:0005134; F:interleukin-2 receptor binding; IPI.
 CC DR GO: GO:0048469; P:cell maturation; IDA.
 CC DR GO: GO:0045078; P:positive regulation of interferon-gamma bio. .; NAS.
 CC DR GO: GO:0042102; P:positive regulation of T cell proliferation; IDA.
 CC DR GO: GO:0007165; P:signal transduction; NAS.
 CC CYTOKINE; Glycoprotein; Signal.
 CC KW CHAIN 1 22 Potential.
 CC FT SIGNAL 23 155 Interleukin-21.
 CC FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
 CC FT DISULFID 64 115 Potential.
 CC FT DISULFID 71 118 Potential.
 CC SQ SEQUENCE 155 AA; 17923 MW; B994A3D1902B914 CRC64;
 QY Query Match 99.3%; Score 706; DB 1; Length 155;
 QY Best Local Similarity 100.0%; Pred. No. 5,1e-57;
 QY Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2 QGDRHMIRKRLIDIVDQKKNVNDLVPEFLPAPBVDVTNCMSAASCFOKQKLSANT 61
 Db 23 QGDRHMIRKRLIDIVDQKKNVNDLVPEFLPAPBVDVTNCMSAASCFOKQKLSANT 82
 QY GNNERIINVSIKKLRKRPSTNAGRROKHLTCSCSYKPKPKELERFKSLIQKIH 121
 Db 83 GNNERIINVSIKKLRKRPSTNAGRROKHLTCSCSYKPKPKELERFKSLIQKIH 142

QY 122 QHLSRTRGSEDS 134
 Db 143 QHLSRTRGSEDS 155
 RESULT 2
 IL21 BOVIN STANDARD; PRT; 146 AA.
 ID IL21 BOVIN AC 076LDS;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 23-NOV-2004, sequence version 2.
 DT 07-FEB-2006, entry version 12.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NCBIOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 18-32, SUBCELLULAR
 RP LOCATION AND TISSUE SPECIFICITY.
 RX Pubmed=12963638; DOI=10.1016/S0165-2427(03)00106-5;
 RA Muneta Y., Kikuma R., Yoshitara K., Mori Y.;
 RT "Cloning, expression, and tissue distribution of bovine interleukin-
 RT 21.";
 RL Vet. Immunol. Immunopathol. 95:73-80(2003).
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed in spleen, but not in the brain,
 CC heart, kidney, liver, and lung.
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL: AB073021; BA087747.1; ALT_INIT; mRNA.
 CC KW CYTOKINE; Direct protein sequencing; Signal.
 CC FT SIGNAL 1 17 Probable.
 CC FT CHAIN 18 146 Interleukin-21.
 CC FT DISULFID 64 115 /Frid=PRO_0000015503.
 CC FT DISULFID 71 118 Potential.
 CC SQ SEQUENCE 146 AA; 16948 MW; 696566DA73F4BB8C CRC64;
 QY Query Match 75.2%; Score 535; DB 1; Length 146;
 QY Best Local Similarity 80.6%; Pred. No. 2.7e-41;
 QY Matches 100; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 Db 2 QGDRHMIRKRLIDIVDQKKNVNDLVPEFLPAPBVDVTNCMSAASCFOKQKLSANT 61
 Db 23 QGDRHMIRKRLIDIVDQKKNVNDLVPEFLPAPBVDVTNCMSAASCFOKQKLSANT 82
 QY GNNERIINVSIKKLRKRPSTNAGRROKHLTCSCSYKPKPKELERFKSLIQKIH 121
 Db 83 GNNERIINVSIKKLRKRPSTNAGRROKHLTCSCSYKPKPKELERFKSLIQKIH 142
 QY 122 QHLS 125
 Db 143 QHLS 146
 RESULT 3

IL21_PIG STANDARD; PRT; 146 AA.
 ID IL21_PIG
 AC 076LUG;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 23-NOV-2004, sequence version 2.
 DT 07-FEB-2006, entry version 12.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND SUBCELLULAR LOCATION.
 RX PubMed=15107555; DOI=10.1292/jvme.66.269;
 RA Muneta Y., Kikuna R., Uenishi H., Hoshino T., Yoshihara K., Tanaka M., Hamashima N., Mori Y.;
 RT "Molecular cloning, expression and biological function of porcine interleukin-21.";
 RL J. Vet. Med. Sci. 66:269-275(2004).
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response may inhibit dendritic cells (DC) activation and maturation.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 DR EMBL; AB073020; BAD11128.1; ALT_INIT; mRNA.
 KM CYtokine; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 146 Interleukin-21.
 FT DISULFID 64 115 /FTID=PRO_0000015508.
 FT DISULFID 71 118 Potential.
 SQ SEQUENCE 146 AA; 16833 MW; 835C63B716230BD1 CRC64;
 Query Match 73.7%; Score 524; DB 1; Length 146;
 Best Local Similarity 80.6%; Pred. No. 2.8e-40;
 Matches 100; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 QY 2 QGQDRHMRKQLDIYDQKNYNDLVPEFLPAPEVETNCWSPSCFOKQKLSANT 61
 DB 23 QGQDRLLRLRQLDIYDQKNYNDLVPEFLPAPEVETNCWSPSCFOKQKLSANT 82
 QY 62 GNNERIINVSIKLKRKPPSTNAGRQKHRLTSPSCSYEKPPKPEFLERKSLIQKNIH 121
 DB 83 GDNKKIINVLTKQKRLPPTNAGRQKHRLTSPSCSYEKPPKPEFLERKSLIQKNIH 142
 QY 122 QHLS 125
 DB 143 QHLS 146
 RESULT 4
 IL21_CANPA STANDARD; PRT; 146 AA.
 ID IL21_CANPA
 AC 06L719;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 NCBI_TaxID=9615;
 AC NCBI [1]
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RC TISUB=Spleen;
 RA Miyake M., Saze K., Haga Y., Yamamoto Y., Iwabuchi S.;
 RT "Molecular cloning of canine interleukin-21 cDNA.";
 RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response may inhibit dendritic cells (DC) activation and maturation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 DR EMBL; AB127975; BAD22569.1; -, mRNA.
 KM Ensembl; ENSGAFG0000004004; Canis familiaris.
 KW Cytokine; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 146 Interleukin-21.
 FT DISULFID 64 115 /FTID=PRO_0000015504.
 FT DISULFID 71 118 Potential.
 SQ SEQUENCE 146 AA; 16776 MW; FFB8DF836AF219AA CRC64;
 Query Match 72.2%; Score 513; DB 1; Length 146;
 Best Local Similarity 80.6%; Pred. No. 2.9e-39;
 Matches 100; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
 QY 2 QGQDRHMRKQLDIYDQKNYNDLVPEFLPAPEVETNCWSPSCFOKQKLSANT 61
 DB 23 QGQDRLLRLRQLDIYDQKNYNDLVPEFLPAPEVETNCWSPSCFOKQKLSANT 82
 QY 62 GNNERIINVSIKLKRKPPSTNAGRQKHRLTSPSCSYEKPPKPEFLERKSLIQKNIH 121
 DB 83 GDNKKIINVLTKQKRLPPTNAGRQKHRLTSPSCSYEKPPKPEFLERKSLIQKNIH 142
 QY 122 QHLS 125
 DB 143 QHLS 146
 RESULT 5
 IL21_MOUSE STANDARD; PRT; 146 AA.
 ID IL21_MOUSE
 AC 09RS17;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=BALB/c;
 RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
 RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kujiyer J.L., Kramer J.,

RA Conklin D., Preenell S.R., Berry J., Shiota F., Bort S., Hamblly K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.,
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.",
RN Nature 408:57-63(2000).
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=BALB/c;
RA Guobing C., Jun D., Junsong C., Fenshu Z.;
RT "Mouse interleukin 21 can improve the anti-tumor effect of LAK
RT cells.",
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RX FUNCTION, AND SUBCELLULAR LOCATION.
RX PubMed=11970879; DOI=10.1016/S1074-7613(02)00295-9;
RA Kasarian M.T., Whitters M.J., Carter L.L., Lowe L.D., Jusaf J.M.,
RA Deng B., Johnson K.A., Witek J.S., Senices M., Konz R.F.,
RA Wurster A.L., Donaldson D.D., Collins M., Young D.A., Grubbs M.J.,
RT "IL-21 limits NK cell responses and promotes antigen-specific T cell
RT activation: a mediator of the transition from innate to adaptive
RT immunity".
RL Immunity 16:559-569(2002).
RN [4]
RN FUNCTION.
RX PubMed=12893770; DOI=10.1182/blood-2003-03-0669;
RA Brandt K., Bulfone-Paus S., Foster D.C., Rueckert R.;
RT "Interleukin-21 inhibits dendritic cell activation and maturation.",
RL Blood 102:4090-4098(2003).
RN [5]
RN FUNCTION.
RX PubMed=15100251;
RA Pene J., Gauchat J.F., Lecart S., Drouet E., Guglielmi P., Boulay V.,
RA Delwail A., Foster D., Legeron J.C., Yssel H.;
RT "IL-21 is a switch factor for the production of IgG1 and IgG3 by human
RT B cells.",
RL Immunol. 172:5154-5157(2004).
CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells. May play a role in
CC proliferation and maturation of natural killer (NK) cells in
CC synergy with IL15. May regulate proliferation of mature B- and T-
CC cells in response to activating stimuli. In synergy with IL15 and
CC IL18 stimulates interferon gamma production in T-cells and NK
CC cells (by similarity). During T-cell mediated immune response may
CC inhibit dendritic cells (DC) activation and maturation.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the IL-21 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
EMBL: ACP54070; AAC29349.1; -; mRNA.
EMBL: AY428162; AAR06254.1; -; mRNA.
Ensembl: ENSMUSG0000027718; Mus musculus.
MGI: MGI.1890474; IL21.
GO: GO:0005615; C:extracellular space; TAS.
GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IDA.
GO: GO:0045579; P:positive regulation of B cell differentiation; NAS.
GO: GO:0001783; P:programmed cell death, B cells; NAS.
CytoKine; Glycoprotein; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 146 Interleukin-21.
FT FTID=PRO_0000015506.
FT CARBOHYD 85 85 /FTID=PRO_0000015506.
FT DISULFID 64 115 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 71 118 Potential.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;
Query Match 56.8%; Score 404; DB 1; Length 146;
Best Local Similarity 62.1%; Pred. No. 3.3e-29;
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 2 QGODRHMIRKQLIDIVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFOKQOLKSANT 61
DB 23 QGPDRLIRLRHLIDIVEQKTYENDLPPELLSAPQVKGHCHEAARACFOKATKPSNP 82
QY 62 GNNERTIIVNSIKLKRRKPSTNAGRRQKRLTCPSCDSEYKKPKFLEPKSLIQMII 121
DB 83 GNNKTFIIDVAQLRRLPARGGKKQKHAKCPSCDSEYKRTPKFLERLKWLQMIH 142
QY 122 QHLS 125
DB 143 QHLS 146
RESULT 6
05USE2 MOUSE PRELIMINARY; PRT; 146 AA.
ID 05USE2_MOUSE
AC 05USE2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Interleukin 21.
GN Name=IL21; ORFName=DN-452A22.7-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
RN NCBI_TaxId=10090;
RP NUCLEOTIDE SEQUENCE.
RA Pandian R.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
EMBL: AL645982; CA126234.1; -; Genomic DNA.
Ensembl: ENSMUSG0000027718; Mus musculus.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;
Query Match 56.8%; Score 404; DB 2; Length 146;
Best Local Similarity 62.1%; Pred. No. 3.3e-29;
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 2 QGODRHMIRKQLIDIVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFOKQOLKSANT 61
DB 23 QGPDRLIRLRHLIDIVEQKTYENDLPPELLSAPQVKGHCHEAARACFOKATKPSNP 82
QY 62 GNNERTIIVNSIKLKRRKPSTNAGRRQKRLTCPSCDSEYKKPKFLEPKSLIQMII 121
DB 83 GNNKTFIIDVAQLRRLPARGGKKQKHAKCPSCDSEYKRTPKFLERLKWLQMIH 142
QY 122 QHLS 125
DB 143 QHLS 146
RESULT 7
IL21_PPRMA STANDARD; PRT; 123 AA.
ID IL21_PPRMA
AC Q80XG2;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Interleukin-21 precursor (IL-21) (Fragment).
GN Name=IL21;
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Cricetidae; Neotominae; Peromyscus.
RN NCBI_TaxId=10042;
RP NUCLEOTIDE SEQUENCE [mRNA].
ID 11

RA Schountz T., Buniger A., Davenport B., Hegg T.,
 RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4
 RL CDNA's";
 CC Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 DR EMBL: AY247761; AAP04420.1; -; mRNA.
 KM Cytokine; Glycoprotein; Signal.
 FT SIGNAL 10 Potential.
 FT CHAIN 11 Interleukin-21.
 FT CARBOHYD 77 /FTid=PRO_0000015507.
 FT DISULFID 56 N-linked (GlcNAc...) (Potential).
 FT DISULFID 63 Potential.
 FT NON_TER 1 Potential.
 FT NON_TER 123 Potential.
 SQ SEQUENCE 123 AA; 13945 MW; 8656C8E95447E34 CRC64;
 Query March 48.4%; Score 344; DB 1; Length 123;
 Best Local Similarity 59.6%; Pred. No. 9.2e-24; Indels 0; Gaps 0;
 Matches 65; Conservative 21; Mismatches 23;
 QY 2 QGQDRHMRMEQLDIDVQLKVVNDLVEFLPAPEDEVETNCESAFSCFQKAKLSANT 61
 DB 15 QRPRLIRLRLHLDVNDVQKLVYDLPDLPAQDVKEHCAHSAFQPKAKLKPRANT 74
 QY 62 GNNERIIVNSIKKLKRKPPSTNAGRQKRLTCPSGDSYEKKPPEFLE 110
 DB 75 GSNKTIISDLVTQLRRRLPATKAEKKQSLVPCSDSEYEKKTPKEFLE 123
 RESULT 8
 ID Q58IU6_CHICK PRELIMINARY; PRT; 145 AA.
 AC Q58IU6;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Interleukin 21.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Shao J., Dong W., Xiang L.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 DR EMBL: AY943833; AAX40651.1; -; mRNA.
 SQ SEQUENCE 145 AA; 16637 MW; E70AB6A568CDABE6 CRC64;
 Query Match 21.0%; Score 149.5; DB 2; Length 145;
 Best Local Similarity 32.0%; Pred. No. 9.4e-06;
 Matches 39; Conservative 20; Mismatches 52; Indels 11; Gaps 4;

QY 9 IRMRQLIDIVDQLKVVNDLVEFLPAPEDEVETNCESAFSCFQKAKLSANTGNNERI 68
 DB 26 MKYQSLSTIDILKDVVDKDVVELHTPEPNPGDGLTAVALCFQNGILKLPKNSQVAT 85
 QY 69 NVSIKKLKRKP--STNAGRQKRLTC-PSGDSYEKKPPEKPELFERFKSLQKMHLS 125
 DB 86 PAKTVKILRRPFLPV-----EEH---CESSCESYERKKQPEFLNFSKLLQKLPKNSA 137
 QY 126 SR 127
 DB 138 ER 139
 RESULT 9
 ID IL15_FELCA STANDARD; PRT; 162 AA.
 AC O97687;
 DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1999, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Interleukin-15 precursor (IL-15).
 GN Name=IL15;
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 CC Felinae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 RN NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=Lymph node;
 RA Barger A.B., Dean G.A., Lavoie A.S.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
 CC lymphocytes. Stimulation by IL-15 requires interaction of IL-2R
 CC with components of IL-2R, including IL-2R beta and probably IL-2R
 CC gamma but not IL-2R alpha (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the IL-15 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 DR EMBL: AF108148; AAD05268.1; -; mRNA.
 DR InterPro: IPR003443; Interleukin_15.
 DR PANTHER: PTHR11323; Interleukin_15; 1.
 DR Pfam: PF02372; IL15; 1.
 KM Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 Potential.
 FT SIGNAL 29 Potential.
 FT PROPEP 30 48 Potential.
 FT CHAIN 49 162 Interleukin-15.
 FT CARBOHYD 104 /FTid=PRO_0000015395.
 FT CARBOHYD 127 N-linked (GlcNAc...) (Potential).
 FT DISULFID 83 N-linked (GlcNAc...) (Potential).
 FT DISULFID 90 Potential.
 FT DISULFID 90 136 Potential.
 SQ SEQUENCE 162 AA; 18412 MW; D8C7CEFF740110DD CRC64;
 Query Match 14.3%; Score 101.5; DB 1; Length 162;
 Best Local Similarity 26.5%; Pred. No. 0.28;
 Matches 31; Conservative 19; Mismatches 48; Indels 19; Gaps 5;
 QY 16 DIVDQLK---NYVNDL-VPEFLPAPEDEVETNCESAFSCF-----QKQKLSANTGNNERI 67
 DB 52 DVIDLKLIDKILDSLHDATLYTESDVHPNCKVYAMKCFLELHVLVSLESKNETIHQTV 111
 QY 68 INVSIIKKLKRKPSTNAGRQKRLT---CPSGDSYEKKPPEKPELFERFKSLQKMHLS 121
 DB 112 ENII-----LANGLSLSNRIITETGCKECELEBKNIKKEFLQSPVHIVQPFIN 160
 RESULT 10
 O6FGX7_HUMAN

ID O6FGX7_HUMAN PRELIMINARY; PRT; 135 AA.
AC O6FGX7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE IL15 protein (Interleukin 15, isoform 2).
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Hallack A., Ebert L., Mkomandinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RC NIH MGC Project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RA Li C.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL: BC100962; AAI00963.1; -; mRNA.
CC EMBL: CR542007; CAG46804.1; -; mRNA.
CC EMBL: AY720442; AAU21241.1; -; mRNA.
CC EMBL: CR541980; CAG46777.1; -; mRNA.
CC EMBL: BC100961; AAI00962.1; -; mRNA.
CC Ensembl: ENSG00000164136; Homo sapiens.
CC GO: GO:0005576; C:extracellular region; IEA.
CC GO: GO:0005126; F:Hemopoietic/interferon-class (D200-domain. .; IEA.
CC GO: GO:0006955; P:Immune response; IEA.
CC InterPro: IPR003443; Interleukin_15.
CC PANTHER: PTHR11323; Interleukin_15; 1.
CC Pfam: Pf02372; IL15; 1.
SQ SEQUENCE 135 AA; 14912 MW; EB44F422096B143B CRC64;

QY 15 IDIVDLKNTVNDLVPEF-----LPADVEYTNCEMSAFSCF-----QKAOLKANTGNNE 65
DB 24 VNVISDLKK-IEBIDLSQMHDAITLYTESDVHPSCKVYAMCFILBQLVSISSGDSIH 82
QY 66 RIIVNSIKLKKRPSPNAGRROKHRLTSPSCSYKKPPKPFLEPKSLLOKKIH 121
DB 83 TWENTLI--IANNLSISNGVNTS--GCKECELSEKNIKETFLQSFWHIVQMFIN 133
RESULT 11
IL15_HUMAN STANDARD; PRT; 162 AA.
AC P40933; O00440; O43512; Q93058; Q9UBA3; Q9UBA3; Swiss-Prot.
DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1995, sequence version 1.
DT 07-FEB-2006, entry version 43.
DE Interleukin-15 precursor (IL-15).
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
RC TISSUE=Bone marrow;
RC MEDLINE=94233380; PubMed=8178155;
RA Grabstein K.H., Eisenman J., Shanebeck K., Rauch C., Srinivasan S.,
RA Pung V., Beers C., Richardson J., Schoenborn M.A., Abdieh M.,
RA Johnson L., Alderson M.R., Watson J.D., Anderson D.M., Gird J.G.;
RT "Cloning of a T cell growth factor that interacts with the beta chain
RT of the interleukin-2 receptor";
RL Science 264:965-968(1994).
RN [2]
RN NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
RA Krause H., Jandrig B., Wernicke C., Bulfone-Paus S., Pohl T.,
RA Diamantstein T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
RC TISSUE=Lung cancer;
RC MEDLINE=96218668; PubMed=8668345;
RX Meazza R., Verdiani S., Biasoni R., Coppolecchia M., Gaggero A.,
RX Orzago A.M., Colombo M.P., Azzone B., Ferrini S.;
RT "Identification of a novel interleukin-15 (IL-15) transcript isoform
RT generated by alternative splicing in human small cell lung cancer cell
RT lines";
RL Oncogene 12:2187-2192(1996).
RN [4]
RN NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
RC TISSUE=Testis;
RC MEDLINE=98070771; PubMed=9405632; DOI=10.1073/pnas.94.26.14444;
RX Tgaya Y., Kury S., Thies T.A., Losi J.M., Azimi N., Hanover J.A.,
RX Barford R.N., Waldmann T.A.;
RT "Generation of secretable and nonsecretable interleukin 15 isoforms
RT through alternate usage of signal peptides";
RL Proc. Natl. Acad. Sci. U.S.A. 94:14444-14449(1997).
RN [5]
RN NUCLEOTIDE SEQUENCE (ISOFORM 3).
RA Meazza R., Ferrini S.;
RT "Expression of two IL-15 mRNA isoforms in human tumors does not
RT correlate with secretion: role of different signal peptides";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM IL15-S48AA).
RC TISSUE=Colon;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lomuello N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumatrat P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Sengerich A., Schein J.E., Jones S.J.W., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 49-162.
RC TISSUE=Epidermis;
RA Sorel M.A., Jacques Y.;
RT "IL15 expression in human keratinocytes.";
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15
CC with components of IL-2R alpha, including IL-2R beta and probably IL-2R
CC gamma but not IL-2R alpha.
CC -1- SUBCELLULAR LOCATION: Secreted (IL15-S48AA). IL15-S21AA is not
CC secreted, but rather is stored intracellularly, appearing in the
CC nucleus and cytoplasmic components.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=IL15-S48AA;
CC IsoId=P40933-1; Sequence=Displayed;
CC Name=IL15-S21AA;
CC IsoId=P40933-2; Sequence=VSP_002660;
CC Name=3;
CC IsoId=P40933-3; Sequence=VSP_002661;
CC -1- TISSUE SPECIFICITY: Most abundant in placenta and skeletal muscle.
CC It is also detected in the heart, lung, liver and kidney. IL15-
CC S21AA is preferentially expressed in tissues such as testis and
CC thymus.
CC -1- SIMILARITY: Belongs to the IL-15 family.
CC -1- DATABASE: NAME=Red Systems' cytokine source book; IL15;
CC WWW="http://www.indyeteams.com/asp/g_atebuilder.asp?bodyid=209".
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License

DR EMBL: BC100963; AA10964.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006555; P:immune response; IEA.
SQ SEQUENCE 162 AA, 18086 MW, 0CE0520CD837952 CRC64;

Query Match 14.0%; Score 99.5; DB 2; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.43;
Matches 30; Conservative 22; Mismatches 48; Indels 15; Gaps 5;

QY 15 IDIVDQKNYNDVLPF-----LPAPDEVTCNCSAFSCF-----QKAOLKSANTGNNE 65
DB 51 VNVISDIKK-IEDLIQSMHIDATLYTESDHPSCVKYAMKCFLELQVSIIESGDASIH 109
DB 110 TVENLII--LANNSLSSNGVNTS--GCKECELKEKNITEFLQSFVHIQMFIN 160

RESULT 13
IL15_RABIT STANDARD; PRT; 162 AA.
AC Q3Y568;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 27-SEP-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Interleukin-15 precursor (IL-15).
GN Name=IL15;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
[1]
NUCLEOTIDE SEQUENCE [mRNA], AND TISSUE SPECIFICITY.
RX PubMed=15978671; DOI=10.1016/j.yetimm.2005.04.013;
RA Xiong C., Hixson P.M., Mendoza L.H., Smith C.W.;
RT "Cloning and expression of rabbit interleukin-15.";
RL Vet. Immunol. Immunopathol. 107:131-141(2005).
CC -!- FUNCTION: Cytokine that stimulates the proliferation of T-
CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15
CC with components of IL-2R, including IL-2R beta and probably IL-2R
CC gamma but not IL-2R alpha (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- TISSUE SPECIFICITY: Expressed in many tissues including heart,
CC spleen, lung, liver, muscle and kidney (at mRNA level). Expressed
CC in many tissues including heart, spleen, lung, liver, muscle and
CC kidney (at protein level).
CC -!- SIMILARITY: Belongs to the IL-15 family.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License

DR EMBL: DQ157452; AA282803.1; -; mRNA.
DR InterPro: IPR003443; Interleukin_15.
DR PANTHER: PTHR11323; Interleukin_15; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 48 Potential.
FT CHAIN 49 162 /FTid=PRO_0000043393.
FT FTid=PRO_0000043394.
FT CARBOHYD 108 108 /FTid=PRO_0000043394. (Potential).
FT CARBOHYD 119 119 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 127 127 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 83 133 Potential.
FT FTid=PRO_0000043393. Potential.
SQ SEQUENCE 162 AA, 18330 MW, 6F9C7C129FB64B9 CRC64;

Query Match 13.9%; Score 98.5; DB 1; Length 162;
Best Local Similarity 27.1%; Pred. No. 0.54;
Matches 32; Conservative 17; Mismatches 48; Indels 21; Gaps 5;

QY 16 DIYDQKNYNDVLPF-----LPAPDEVTCNCSAFSCF-----QKAOLKSANTGNNE 66
DB 52 DIYDQKNYNDVLPF-----LPAPDEVTCNCSAFSCF-----QKAOLKSANTGNNE 110
DB 111 VNNIILANTSLSSKGNVTS-----GCKECELKEKNITEFLQSFVHIQMFIN 160

Query 67 IINVSII--KKLKRKPPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQKMH 121
DB 111 VNNIILANTSLSSKGNVTS-----GCKECELKEKNITEFLQSFVHIQMFIN 160

RESULT 14
Q5W7F5_BRARE PRELIMINARY; PRT; 162 AA.
ID Q5W7F5_BRARE
AC Q5W7F5;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Interleukin-15 1.
GN Name=il15; Synonyms=IL-15 1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hama S., Ram S., Sakai M.;
RT "Cloning of interleukin 15 genes from zebrafish.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License

DR EMBL: AB194244; BAD69558.1; -; mRNA.
DR Ensembl: ENSDARG0000007743; Danio rerio.
DR ZFIN: ZDB-GENE-041111-173; Ilm:7142994.
SQ SEQUENCE 162 AA, 18924 MW, F0C9F389C7A392DE CRC64;

Query Match 13.6%; Score 96.5; DB 2; Length 162;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 29; Conservative 26; Mismatches 40; Indels 25; Gaps 5;

QY 12 RQIIDIYDQ-----IKNYNDVLPFELPAPDEVTCNCSAFSCF-----KAOLKSA 59
DB 48 RESVEMKQIAAKLANNVNDQM--MYTPQANRK--NCKSTITTCAPFVSVALSVIQLVSL 105
QY 60 NTGNNERIIINVSIIKKLKRKPPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQKMH 119
DB 106 AFRQGLRIILNRVYKRL-----QDEMCKKPCVCELYKESYTFPLNTIQLHLEQM 154

RESULT 15
Q32PM5_BRARE PRELIMINARY; PRT; 160 AA.
ID Q32PM5_BRARE
AC Q32PM5;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE Zgc:123044.
GN ORFNames=zgc:123044;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Search completed: August 14, 2006, 21:51:42
Job time : 304 secs

THIS PAGE LEFT BLANK